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Enter an option number to view information or to connect to an online
 service.  Enter a BEGIN command plus a file number to search a database
(e.g., B1 for ERIC).
?b 155

       10dec02 17:04:05 User228206 Session D1890.1
            $0.00    0.162 DialUnits FileHomeBase
     $0.00  Estimated cost FileHomeBase
     $0.00  Estimated cost this search
     $0.00  Estimated total session cost   0.162 DialUnits

### Status: Break Sent.

?s (plasmod? or malar?)/ti and plastid?/ti
           11588  PLASMOD?/TI
           17075  MALAR?/TI
             900  PLASTID?/TI
      S1      20  (PLASMOD? OR MALAR?)/TI AND PLASTID?/TI
?t s1/9/all

 1/9/1
DIALOG(R)File 155:MEDLINE(R)
```

Sequence of the small subunit ribosomal RNA gene expressed in the bloodstream stages of Plasmodium berghei: evolutionary implications.
Nov 1986
Tags: Animal; Comparative Study; Support, U.S. Gov't, P.H.S.
Descriptors: Genes; * **Plasmodium berghei** --genetics--GE; * **RNA** , Ribosomal--genetics--GE; Base Sequence; Evolution; Phylogeny
Molecular Sequence Databank No.: GENBANK/M14599
CAS Registry No.: 0 (RNA, Ribosomal)

A latent intron-encoded maturase is also an endonuclease needed for intron mobility.

Wenzlau J M; Saldanha R J; Butow R A; Perlman P S
Department of Molecular Genetics, Ohio State University, Columbus 43210.

Cell (UNITED STATES) Feb 10 1989, 56 (3) p421-30, ISSN 0092-8674
Journal Code: 0413066
Contract/Grant No.: GM35510; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Some yeast mitochondrial introns encode proteins that promote either splicing (maturases) or intron propagation via gene conversion (the fit1 endonuclease). We surveyed introns in the **cox1** gene for their ability to engage in gene conversion and found that the group I intron, al4 alpha, was efficiently transmitted to genes lacking it. An endonucleolytic cleavage is detectable in recipient DNA molecules near the site of intron insertion in vivo and in vitro. Conversion is dependent on an intact al4 alpha open reading frame. This intron product is a latent maturase, but these data show that it is also a potent endonuclease involved in recombination. Dual function proteins that cleave DNA and facilitate RNA splicing may have played a pivotal role in the propagation and tolerance of introns.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
Descriptors: *Endoribonucleases--genetics--GE; *Genes, Fungal; *Introns; *Nucleotidyltransferases--genetics--GE; *Saccharomyces cerevisiae--genetics --GE; Base Sequence; Crosses, Genetic; DNA, Mitochondrial--genetics--GE; Molecular Sequence Data; Plasmids
CAS Registry No.: 0 (DNA, Mitochondrial); 0 (Plasmids)
Enzyme No.: EC 2.7.7 (Nucleotidyltransferases); EC 2.7.7.- (mRNA maturase); EC 3.1.- (Endoribonucleases)
Record Date Created: 19890317

The structural genes encoding CO dehydrogenase subunits (cox L, M and S) in Pseudomonas carboxydovorans OM5 reside on plasmid pHCG3 and are, with the exception of Streptomyces thermoautotrophicus, conserved in carboxydotrophic bacteria.

Hugendieck I; Meyer O

Lehrstuhl fur Mikrobiologie, Universitat Bayreuth, Federal Republic of Germany.

Archives of microbiology (GERMANY) 1992, 157 (3) p301-4, ISSN 0302-8933 Journal Code: 0410427

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Employing deoxyoligonucleotide probes and Southern hybridizations, we have examined in carboxydotrophic bacteria the localization on the genome of genes encoding the large, medium and small subunits of CO dehydrogenase (**coxL** , M and S, respectively). In Pseudomonas carboxydovorans OM5 **coxL** , M and S were identified on the plasmid pHCG3; they were absent on the chromosome. This was evident from positive hybridizations with plasmid DNA of the wild-type strain OM5 and the absence of hybridizations with chromosomal DNA from the plasmid cured mutant strain OM5-12. The genes **coxL** , M and S were found on plasmids in all other plasmid-containing carboxydotrophic bacteria e.g. Alcaligenes carboxydus, Azomonas B1, Pseudomonas carboxydoflava, Pseudomonas carboxydovorans OM2 and OM4. Cox L, M and S could be identified on the chromosome of the plasmid-free bacteria Arthrobacter 11/x, Bacillus schlegelii, Pseudomonas carboxydohydrogena, and Pseudomonas carboxydovorans OM3. These results essentially confirm and extend former reports that cox genes are rather conserved among carboxydotrophic bacteria of distinct taxonomic position. However, Streptomyces thermoautotrophicus is an noteworthy exception since none of the three cox genes could be detected. This refers to a new type of CO dehydrogenase and is in accord with results indicating that the S. thermoautotrophicus CO dehydrogenase has an unusual electron acceptor specificity and some other properties setting it apart from the 'classical' CO dehydrogenases.

Tags: Comparative Study; Support, Non-U.S. Gov't

Detection of DNA sequences in Plasmodium berghei by means of in situ hybridization.

Obst M; Cornelissen A W

Max-Planck-Institut fur Biologie, Molecular Parasitology Unit, Tubingen, Federal Republic of Germany.

Histochemistry (GERMANY, WEST) 1990, 94 (1) p101-7, ISSN 0301-5564 Journal Code: 0411300

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A non-radioactive in situ hybridization technique, used to map unique DNA sequences to plant chromosomes, has been adapted for the localization of specific DNA sequences in nuclei of Plasmodium berghei. After hybridization using probes labeled with biotin-11-dUTP, the formed DNA/DNA hybrids were detected by fluorescence microscopy using a specific double-layer antibody technique. Besides its high resolution, this procedure is characterized by a high sensitivity, allowing the detection of a unique sequence as small as 2.5 kb.

Tags: Animal; Support, Non-U.S. Gov't

Descriptors: DNA--analysis--AN; * **DNA Probes** ; *Nucleic Acid **Hybridization** ; * **Plasmodium** berghei--genetics--GE; Biotin; Cell Nucleus --analysis--AN; Immunohistochemistry

CAS Registry No.: 0 (DNA Probes); 58-85-5 (Biotin); 9007-49-2 (DNA)

Record Date Created: 19900718

An mRNA maturase is encoded by the first intron of the mitochondrial gene for the subunit I of cytochrome oxidase in S. cerevisiae.

Carignani G; Groudinsky O; Frezza D; Schiavon E; Bergantino E; Slonimski P P

Cell (UNITED STATES) Dec 1983, 35 (3 Pt 2) p733-42, ISSN 0092-8674 Journal Code: 0413066

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

We have localized ten oxi3- mutations in the first, al1, intron of the **cox1** gene. All are splicing deficient, being unable to excise the intron. Complementation experiments disclose several domains in the intron al1: the 5'-proximal and 3'-proximal domains harbor cis-dominant mutations, while trans-recessive ones are located in the intron's open reading frame. Comprehensive analyses of allele-specific polypeptides accumulating in mutants show that they result from the translation of the intron's ORF. We conclude that a specific mRNA maturase involved in splicing of oxidase mRNA is encoded by the intron al1 in a manner similar to the cytochrome b mRNA maturase.

Tags: Support, Non-U.S. Gov't

Descriptors: *Cytochrome-c Oxidase--genetics--GE; *DNA, Mitochondrial --genetics--GE; *Saccharomyces cerevisiae--genetics--GE; Chromosome Mapping ; Genes, Structural; Macromolecular Systems; Molecular Weight; Nucleotidyltransferases--genetics--GE; Transcription, Genetic; Translation, Genetic

CAS Registry No.: 0 (DNA, Mitochondrial); 0 (Macromolecular Systems)

Enzyme No.: EC 1.9.3.1 (Cytochrome-c Oxidase); EC 2.7.7 (Nucleotidyltransferases); EC 2.7.7.- (mRNA maturase)

Record Date Created: 19840215

Novel hybrid maturases in unstable pseudorevertants of maturaseless mutants of yeast mitochondrial DNA.

Anziano P Q; Moran J V; Gerber D; Perlman P S

Molecular Cellular and Developmental Biology Program, Ohio State University, Columbus 43210-1292.

Nucleic acids research (ENGLAND) Jun 11 1990, 18 (11) p3233-9, ISSN 0305-1048 Journal Code: 0411011

Contract/Grant No.: GM35510; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Unstable pseudorevertants of mitochondrial mutants of Saccharomyces cerevisiae lacking the maturase function encoded by the fourth intron of the cytochrome b gene (bI4) were isolated. They were found to be heteroplasmic cells owing their regained ability to respire (and grow on glycerol medium) to the presence of a rearranged (rho-) mtDNA that contains an in-frame fusion of the reading frames of the group I introns bI4 and intron 4 alpha of the **coxl** gene encoding subunit I of cytochrome c oxidase (aI4 alpha). The products of those gene fusions suppress the bI4 maturase deficiency still present in those heteroplasmic cells. Similar heteroplasmic pseudorevertants of a group II maturaseless mutant of the first intron of the coxI gene were characterized; they result from partial deletion of the coxI gene that fuses the reading frames of introns 1 and 2. These heteroplasms provide independent support for the existence of RNA maturases encoded by group I and group II introns. Also, since the petite/mit- heteroplasms arise spontaneously at very high frequencies they provide a system that can be used to obtain mutants unable to form or maintain heteroplasmic cells.

Tags: Support, U.S. Gov't, P.H.S.

Molecular characterization of the gene cluster coxMSL encoding the molybdenum-containing carbon monoxide dehydrogenase of Oligotropha carboxidovorans.

Schubel U; Kraut M; Morsdorf G; Meyer O
Lehrstuhl fur Mikrobiologie, Universitat Bayreuth, Germany.

Journal of bacteriology (UNITED STATES) Apr 1995, 177 (8) p2197-203, ISSN 0021-9193 Journal Code: 2985120R
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The CO dehydrogenase structural genes (cox) and orf4 are clustered in the transcriptional order coxM--> coxS--> **coxL** --> orf4 on the 128-kb megaplasmid pHCG3 of the carboxidotroph Oligotropha carboxidovorans OM5. Sequence analysis suggested association of molybdopterin cytosine dinucleotide and flavin adenine dinucleotide with **CoxL** and of the [2Fe-2S] clusters with CoxS.

Tags: Comparative Study; Support, Non-U.S. Gov't
Descriptors: *Aldehyde Oxidoreductases--genetics--GE; *Genes, Bac

09062418 96422590 PMID: 8825207

Identification of a Plasmodium berghei antigen sharing common features with P. falciparum **and P. chabaudi parasitophorous-vacuole membrane antigens.**

Tan T M; Goh K L; Binh L N; Ting R C; Kara U A

Institute of Molecular and Cell Biology, National University of Singapore.

Parasitology research (GERMANY) 1996, 82 (2) p130-35, ISSN 0932-0113 Journal Code: 8703571

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

On the basis of immunological cross-reactivity, we identified a 43-kDa Plasmodium **berghei** antigen with homology to the exp-1 antigen from P. falciparium. The P. **berghei** antigen was recognized by an antibody directed against an epitope on the C-terminus of the P. **falciparum** exp-1 protein. This antigen is localized on the surface of the parasite and shares peptide sequence homology with the P. chabudi antigen Ag3008. To investigate further the role of the P. **berghei** antigen, we designed antisense phosphorothioate oligodeoxynucleotides (PS oligos) complementary to sequences of the exp-1 mRNA from P. **falciparum** . The PS oligos were capable of inhibiting the development of P. **falciparum** in vitro by 47%. In vivo, experiments in mice showed that the same PS oligos had the potential to extend the life span of mice infected with P. **berghei** by a factor of 2-4. The immunological cross-reactivity and the antisense inhibition of P. **berghei** parasite development in vivo indicate that this antigen may be a homologue of exp-1 from P. **falciparum** that has functional importance for parasite survival.

Tags: Animal

Descriptors: *Antigens, Protozoan--immunology--IM; *Plasmodium berghei --immunology--IM; *Plasmodium chabaudi--immunology--IM; *Plasmodium falciparum--immunology--IM; Amino Acid Sequence; Antimalarials --pharmacology--PD; Base Sequence; DNA, Protozoan--genetics--GE; Malaria, Falciparum--drug therapy--DT; Malaria, Falciparum--immunology--IM; Malaria, Falciparum--pathology--PA; Mice; Molecular Sequence Data; Oligonucleotides--pharmacology--PD; Peptides--chemistry--CH; Plasmodium falciparum--drug effects--DE

CAS Registry No.: 0 (Antigens, Protozoan); 0 (Antimalarials); 0 (DNA, Protozoan); 0 (Oligonucleotides); 0 (Peptides); 0 (QF116 antigen)

Record Date Created: 19961205

07810768 93341571 PMID: 8341321

Molecular cloning and localization of an abundant novel protein of Plasmodium berghei.

Uparanukraw P; Toyoshima T; Aikawa M; Kumar N

Department of Immunology and Infectious Diseases, School of Hygiene and Public Health, Johns Hopkins University, Baltimore, MD 21205.

Molecular and biochemical parasitology (NETHERLANDS) Jun 1993, 59 (2) p223-34, ISSN 0166-6851 Journal Code: 8006324

Contract/Grant No.: AI31589; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Screening of Plasmodium **berghei** genomic libraries using **DNA** insert corresponding to the 3' half of P. **falciparum** 70-kDa heat shock protein **gene** identified several abundant clones which represent a novel **gene** in the parasite. The complete sequence was obtained using an approach based on inverse polymerase chain reaction. Analysis of the deduced amino acid sequence revealed the presence of 19 imperfect repeats of the sequence Gly-Gly-Met-Pro toward the carboxy terminus. Except for the similar sequence repeated seven times in the malarial 70-kDa heat shock protein, the sequence of the cloned **gene** product is very different. Moreover, the sequence also revealed acidic and basic domains in the protein which are more than 60% similar in sequence to functional domains present in numerous **DNA** binding transcription factors. A 56-kDa protein was identified by immunoprecipitation from labeled P. berghei extract using antisera raised in mice against **gene** products expressed in Escherichia coli. The protein is present in all the different life cycle stages of the parasites as revealed by immunoelectron microscopy.

Tags: Animal; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.

Descriptors: Heat-Shock Proteins--biosynthesis--BI; *Plasmodium

08651393 96002381 PMID: 7565129

Attempted isolation of the gene **encoding the 21 Kd Plasmodium berghei ookinete transmission blocking antigen from Plasmodium yoelli and Plasmodium vivax.**

Barker G C; Rodriguez M H; Sinden R E
Department of Biology, Imperial College, London, England.

Memorias do Instituto Oswaldo Cruz (BRAZIL) 1994, 89 Suppl 2 p37-41, ISSN 0074-0276 Journal Code: 7502619
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The 21kD ookinete antigen of Plasmodium **berghei** (Pbs 21) has been shown to elicit an effective and long lasting transmission blocking immune response in mice. Having cloned and sequenced this antigen (Paton et al. 1993) the sequence was compared to the **genes** of the same family previously identified in P. **falciparum** , P. gallinaceum (Kaslow et al. 1989) and P. reichenowi (Lal et al. 1990). Four conserved areas were identified in this comparison, to which degenerate oligonucleotides were designed. PCR amplification and screening of genomic libraries was then carried out using these oligonucleotides. The P. yoelii **gene** was successfully cloned and a number of novel P. vivax **genes** identified but the P. vivax homologue of Pbs21 remains elusive.

Tags: Animal; Comparative Study
Descriptors: **Genes** , Protozoan-- **genetics** --GE; *Plasmodium-- **genetics** --GE; Base Sequence; Chromosome Mapping; Gene Library; Genetic Code; Mice; Molecular Sequence Data; Plasmodium berghei--genetics--GE; Plasmodium vivax --genetics--GE; Plasmodium yoelii--genetics--GE; Polymerase Chain Reaction; Sequence Analysis, **DNA** --methods--MT
Record Date Created: 19951020

A chromatin-associated protein is encoded in a genomic region highly conserved in the Plasmodium genus.

Birago C; Pace T; Barca S; Picci L; Ponzi M

Laboratorio di Biologia Cellulare, Istituto Superiore di Sanita, Rome, Italy.

Molecular and biochemical parasitology (NETHERLANDS) Oct 1 1996, 80 (2) p193-202, ISSN 0166-6851 Journal Code: 8006324

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A single copy **gene** , pbB7, encoding a putative 26 kDa acidic protein has been isolated from Plasmodium berghei and appears to be part of a genomic region well conserved within the Plasmodium genus. The deduced amino acid sequence exhibits significant blocks of similarity with nucleosome assembly proteins from yeast and man. The nuclear localization of the natural protein and its close association with chromatin during the entire erythrocytic cycle of the parasite have been demonstrated using specific monoclonal antibodies against the pbB7 product expressed in Escherichia coli. These results suggest an involvement of this nuclear factor in the dynamics of chromatin packaging.

Tags: Animal; Human; Support, Non-U.S. Gov't

Descriptors: Chromatin-- **genetics** --GE; *Plasmodium-- **genetics** --GE; *Protozoan Proteins-- **genetics** --GE; Amino Acid Sequence; Antibodies, Monoclonal; Base Sequence; Chromatin--immunology--IM; Chromatin --metabolism--ME; Conserved Sequence; DNA Primers--genetics--GE; Escherichia coli--genetics--GE; Genes, Protozoan; Genome, Protozoan; Linkage (Genetics); Mice; Molecular Sequence Data; Plasmodium--immunology --IM; Plasmodium--metabolism--ME; Plasmodium berghei--genetics--GE; Plasmodium berghei--immunology--IM; Plasmodium **berghei** --metabolism--ME; Plasmodium **falciparum** -- **genetics** --GE; Plasmodium **falciparum** --immunology--IM; Plasmodium **falciparum** --metabolism--ME; Protozoan Proteins--immunology--IM; Protozoan Proteins--metabolism--ME; Recombinant Proteins-- **genetics** --GE; Recombinant Proteins--immunology--IM;

Chromosomal **polymorphism and sexual differentiation in Plasmodium.**

Ponzi M; Alano P; Scotti R; Roca L

Laboratorio di Biologia Cellulare, Istituto Superiore di Sanita, Roma, Italia.

Parassitologia (ITALY) Jul 1993, 35 Suppl p87-9, ISSN 0048-2951
Journal Code: 0413724

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The correlation observed in several instances between the loss of ability to produce gametocytes and **chromosomal** rearrangements, prompted us to investigate in further detail the molecular bases of **chromosomal** polymorphism in Plasmodium. **Generation** of polymorphic karyotypes in Plasmodium involves important rearrangements, mostly occurring in subtelomeric position. Detailed analysis on the organisation of these regions have been carried out on the rodent malaria P. **berghei** and the human malaria P. **falciparum** . A 2.3kb sequence, tandemly organised in long clusters is shared by many P. **berghei** **chromosomal** ends. Variations in the copy number of this "module" account for most of the observed polymorphisms. In a P. **falciparum** cloned line (3D7) a common region spanning at least 40 kb, is present. It does not contain any repetitive structure other than the rep20 cluster, that appears to be completely contained within the common region. Notwithstanding the structural differences, human and rodent Plasmodia share the common feature of possessing long subtelomeric regions showing, thus, a homology between the different **chromosomes** .

Tags: Animal; Comparative Study; Female; Male

Descriptors: *Chromosomes--ultrastructure--UL; *Plasmodium berghei --genetics--GE; *Plasmodium falciparum--genetics--GE; *Polymorphism (Genetics); Chromosome Aberrations; Chromosome Deletion; Chromosome Mapping ; DNA, Protozoan--genetics--GE; Plasmodium berghei--physiology--PH; Plasmodium falciparum--physiology--PH; Repetitive Sequences, Nucleic Acid; Species Specificity

CAS Registry No.: 0 (DNA, Protozoan)

Record Date Created: 19931216

Phylogenetic relationship among the malaria parasites based on small subunit rRNA gene sequences: monophyletic nature of the human malaria parasite, Plasmodium falciparum.

Qari S H; Shi Y P; Pieniazek N J; Collins W E; Lal A A

Immunology Branch, Centers for Disease Control and Prevention, Atlanta, Georgia 30341, USA.

Molecular phylogenetics and evolution (UNITED STATES) Aug 1996, 6 (1) p157-65, ISSN 1055-7903 Journal Code: 9304400

Contract/Grant No.: 1 UO1 AI37543-01; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

We analyzed the small subunit ribosomal RNA (SSUrRNA) **gene** sequences from 13 malaria species parasitic to humans, chimpanzees/gorillas, Old World monkeys, rodents, birds, and lizards in order to reconstruct the phylogenetic relationships among the Plasmodium species. The SSUrRNA **genes** of Plasmodium vivax and P. ovale were sequenced by the dideoxy method in our laboratory; other sequences were retrived from GenBank. These sequences were aligned with the SSUrRNA **gene** sequence of outgroup species, Paramecium and Toxoplasma. After gaps and ambiguous regions were deleted, the aligned sequences were used for phylogenetic analysis by maximum likelihood and distance methods. The tree defines two major clades, the first with the bird and reptile parasites, the second with the rest of the species. The two bird parasites, P. gallinaceum and P. lophurae, do not closely cluster with human, chimpanzee/gorilla, Old World monkey, or rodent parasites, but cluster with the lizard parasites. P. vivax clusters with three Old World monkey parasites, P. cynomolgi, P. fragile, and P. knowlesi in decreasing order of closeness. P. ovale, while in a separate clade, is more closely related to P. vivax than to P. malarie or P. **falciparum** . P. malariae and P. **berghei** do not closely cluster with any of the other clades or with each other. Statistical analysis proves that the placement of P. **falciparum** in the bird malaria clade is less likely than in the mammalian malaria clade. Our analysis reveals that: (1) human malaria parasites have an evolutionary independent origin; (2) P. falciparum is most closely related to P. reichenowi and did not arise from lateral transfer of a bird parasite, as was previously suggested; and (3) the lizard malaria parasites are true members of the genus Plasmodium.

Tags: Animal; Support, U.S. Gov't, P.H.S.

Descriptors: Phylogeny; *Plasmodium falciparum--genetics--GE; *RNA, Ribosomal-- **genetics** --GE; Base Sequence; Molecular Sequence Data; Plasmodium falciparum--classification--CL; Sequence Alignment; Species Specificity

Molecular Sequence Databank No.: GENBANK/L07560; GENBANK/L08241; GENBANK/L11716; GENBANK/L11717; GENBANK/L48986; GENBANK/L48987; GENBANK/M14599; GENBANK/M19172; GENBANK/M54897; GENBANK/M61722; GENBANK/M61723; GENBANK/U03070; GENBANK/U03079; GENBANK/X03772; GENBANK/X13706; GENBANK/Z25819

CAS Registry No.: 0 (RNA, Ribosomal)

Record Date Created: 19961204

Identification and characterization of a generic DNA probe capable of detecting plasmodial infections in blood.

Ayyanathan K; Datta S
Astra Research Centre India, Malleswaram, Bangalore, India.

Molecular and cellular probes (ENGLAND) Aug 1996, 10 (4) p273-8, ISSN 0890-8508 Journal Code: 8709751
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

DNA-based detection systems are being rapidly adapted for diagnostic technologies. The currently available non-radioactive DNA techniques for malaria detection are primarily based on probes which are species-specific. The major requirement of a cross-species (generic) diagnostics is the identification of an universal probe which is long enough to be used in either PCR amplification or solid state capture of the hybrids, the two principal techniques currently used in the field of non-radioactive DNA detection. This paper describes a **DNA** sequence (pARC 178), originally obtained from P. falciparum genomic library, which is also present in other malarial species. Southern-blot analysis indicates that this sequence is derived from a repetitive **DNA** element. This **DNA** fragment encodes for a small RNA species of approximately 120 bases. PCR **primers** based on this sequence amplifies the expected size (157 bp) product from the genomic **DNA** isolated from P. **falciparum** , P. vivax, P. **berghei** , P. yoelii, P. vinckei and P. chabaudi thus confirming its **generic** nature. The utility of this **probe** is further demonstrated by its capability in successfully detecting P. **falciparum** and P. vivax infections in clinical samples when used in a PCR assay.

Tags: Animal; Human
Descriptors: *DNA Probes; *DNA, Protozoan--blood--BL; *Malaria--diagnosis --DI; *Plasmodium--genetics--GE; *Polymerase Chain Reaction--methods--MT; Base Sequence; Cloning, Molecular; DNA, Protozoan--genetics--GE; Molecular Sequence Data; Plasmodium falciparum--genetics--GE; RNA, Protozoan --analysis--AN; Repetitive Sequences, Nucleic Acid; Sequence Analysis, DNA; Species Specificity
CAS Registry No.: 0 (DNA Probes); 0 (DNA, Protozoan); 0 (RNA, Protozoan)
Record Date Created: 19961227

15/9/51 (Item 51 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

04616221 84300254 PMID: 6382604
Evolutionary relatedness of Plasmodium species as determined by the structure of DNA.
McCutchan T F; Dame J B; Miller L H; Barnwell J
Science (UNITED STATES) Aug 24 1984, 225 (4664) p808-11, ISSN 0036-8075 Journal Code: 0404511
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Malaria parasites can be grouped evolutionarily by analysis of DNA composition and genome arrangement. Those that vary widely with regard to host range, morphology, and biological characteristics fit into only a small number of distinctive groups. The DNA of the human parasite Plasmodium falciparum fits into a group that includes rodent and avian malarias and is unlike the DNA of other primate malaria parasites. The DNA of Plasmodium vivax, which is also a human parasite, fits into a distinctly different group that includes Plasmodium cynomolgi, a parasite of monkeys. The evolutionary lines suggested here appear to be consistent with similarities seen among malaria parasites with regard to gene sequence.
Tags: Animal; Comparative Study
Descriptors: *DNA--analysis--AN; *Evolution; *Plasmodium--classification --CL; Base Composition; Base Sequence; Deoxycytidine--analysis--AN; Deoxyguanosine--analysis--AN; **Nucleic** Acid **Hybridization** ; Plasmodium --genetics--GE; **Plasmodium berghei** --classification--CL; Plasmodium berghei--genetics--GE; Plasmodium falciparum--classification--CL; Plasmodi um falciparum--genetics--GE; Plasmodium vivax--classification--CL; Plasmodium vivax--genetics--GE; Species Specificity
CAS Registry No.: 9007-49-2 (DNA); 951-77-9 (Deoxycytidine); 961-07-9 (Deoxyguanosine)
Record Date Created: 19840924

15/9/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09178514 97079465 PMID: 8921197
A one-step lysis procedure for 18S ribosomal RNA-based diagnosis of infection by Plasmodium species.
Das A; Lal A A; Talwar G P; Hasnain S E; Sinha S
National Institute of Immunology, Aruna Asaf Ali Marg, New Delhi, India.
Analytical biochemistry (UNITED STATES) Oct 15 1996, 241 (2) p262-4, ISSN 0003-2697 Journal Code: 0370535
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Tags: Animal; Human; Support, U.S. Gov't, Non-P.H.S.
Descriptors: Malaria--diagnosis--DI; * **Plasmodium berghei** --genetics--GE; * **RNA** , Ribosomal, 18S--genetics--GE; Nucleic Acid Hybridization
CAS Registry No.: 0 (RNA, Ribosomal, 18S)
Record Date Created: 19970212

15/9/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08493089 95258085 PMID: 7739674
Conserved location of genes on polymorphic chromosomes of four species of malaria parasites.
Janse C J; Carlton J M; Walliker D; Waters A P
Laboratory for Parasitology, University of Leiden, The Netherlands.

Molecular and biochemical parasitology (NETHERLANDS) Dec 1994, 68 (2) p285-96, ISSN 0166-6851 Journal Code: 8006324
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The number of chromosomes and the chromosomal location and linkage of more than 50 probes, mainly of genes, have been established in four species of Plasmodium which infect African murine rodents. We expected that the location and linkage of genes would not be conserved between these species of malaria parasites since extensive inter- and intraspecific size differences of the chromosomes existed and large scale internal rearrangements and chromosome translocations in parasites from laboratory lines had been reported. Our study showed that all four species contained 14 chromosomes, ranging in size between 0.5 and 3.5 Mb, which showed extensive size polymorphisms. The location and linkage of the genes on the polymorphic chromosomes, however, was conserved and nearly identical between these species. These results indicate that size polymorphisms of the chromosomes are more likely due to variation in non-coding (subtelomeric, repeat) sequences and show that a high plasticity of internal regions of chromosomes that may exist does not frequently affect chromosomal location and linkage of genes.

Tags: Animal; Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Chromosome Mapping; *Chromosomes--genetics--GE; *Genes, Protozoan--genetics--GE; *Malaria--parasitology--PS; *Plasmodium--genetics --GE; Electrophoresis, Gel, Pulsed-Field; Gene Rearrangement; Linkage (Genetics); Mice; Molecular **Probes** ; **Plasmodium** berghei--genetics--GE; Plasmodium chabaudi--genetics--GE; Plasmodium yoelii--genetics--GE; Polymorphism (Genetics)

CAS Registry No.: 0 (Molecular Probes)
Record Date Created: 19950602

15/9/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08493086 95258082 PMID: 7739671

Differential expression in blood stages of the gene coding for the 21-kilodalton surface protein of ookinetes of Plasmodium berghei as detected by RNA in situ hybridisation.

Vervenne R A; Dirks R W; Ramesar J; Waters A P; Janse C J
Department of Parasitology, University of Leiden, The Netherlands.
Molecular and biochemical parasitology (NETHERLANDS) Dec 1994, 68 (2) p259-66, ISSN 0166-6851 Journal Code: 8006324
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The developmentally regulated transcription of the gene encoding the ookinete surface protein, Pbs21, has been investigated in the rodent malaria parasite, Plasmodium berghei, by RNA in situ hybridisation using fluorescently labelled DNA probes. We used a procedure that will allow the visualisation of cytoplasmic mRNA in the parasite and of high copy DNA repeats in the nucleus. Specific hybridisation to Pbs21 mRNA occurred in the cytoplasm of female gametocytes, zygotes and ookinetes, while asexual blood stages, male gametocytes and gametes showed no fluorescence. Analysis of the transcription of the Pbs21 gene during blood stage development in two tightly synchronised parasite clones using the same methodology revealed that transcription is restricted to sexual stages and is initiated in immature gametocytes at 19 h post invasion (hpi). At this point in development it is not yet possible to discriminate between the morphology of asexual trophozoites and immature gametocytes. At 24 hpi approximately 50% of the gametocytes transcribed the Pbs21 gene and the morphology of these gametocytes was identical and female. The distribution of the mRNA encoding Pbs21 confirmed that post-transcriptional control of expression occurred in the cytoplasm by repression of translation and not through delayed transport of the message to the cytoplasm. The transcription of the

Pbs21 gene is the earliest demonstrated event in gametocytogenesis in rodent malaria species to date.
Tags: Animal; Female; Male; Support, Non-U.S. Gov't
Descriptors: *Antigens, Surface--biosynthesis--BI; *Erythrocytes --parasitology--PS; *Genes, Protozoan; *Plasmodium berghei--immunology--IM; *Protozoan Proteins--biosynthesis--BI; *RNA, Protozoan--analysis--AN; Antigens, Protozoan--biosynthesis--BI; Antigens, Protozoan--genetics--GE; Antigens, Surface--genetics--GE; DNA Probes; Fluorescent Dyes; Gene Expression Regulation--physiology--PH; In Situ **Hybridization** , Fluorescence; Mice; **Plasmodium berghei** --genetics--GE; Protozoan Proteins --genetics--GE; RNA, Messenger--analysis--AN; RNA, Protozoan--isolation and purification--IP; Rats
CAS Registry No.: 0 (Antigens, Protozoan); 0 (Antigens, Surface); 0 (DNA Probes); 0 (Fluorescent Dyes); 0 (Protozoan Proteins); 0 (RNA, Messenger); 0 (RNA, Protozoan); 0 (ookinete surface antigen Pbs21, Plasmodium)
Record Date Created: 19950602

15/9/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08263247 95020922 PMID: 7935181
[A comparative restriction analysis of the DNA of strains of the malarial parasite sensitive and resistant to chloroquine]
Sravnitel'nyi restriktsionnyi analiz DNK shtammov maliariinogo parazita chuvstvitel'nogo i rezistentnykh k khlorokhinu.
Pankova T G; Igonina T M; Klimova E R; Maier T V
Meditsinskaia parazitologiia i parazitarnye bolezni (RUSSIA) Apr-Jun 1994, (2) p13-9, ISSN 0025-8326 Journal Code: 0376635
Document type: Journal Article ; English Abstract
Languages: RUSSIAN
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
A comparative restriction analysis was made for DNA in malaria parasites, strain H sensitive to chloroquinone, strain LNK-65 with spontaneously occurred resistance to the agent, and breeding strain LNK-65 ChlR highly resistant to it. DNA hydrolysis with EcoR1, HindIII, and BamH1 endonucleases revealed permanent differences in the DNA restriction pattern of malaria parasites. There were additional restriction bands as part of DNA restricts in the strain LNK-65 Chl bred from LNK-65 for high resistance to chloroquine on EcoR1-, HindIII-, and BamH1-hydrolysis. Great differences in the DNA restriction pattern in the strains H and LNK-65 are likely to be due to their belonging to various strains, such as P.berghei and P.yoelii, respectively. Comparison of the DNA restriction pattern of the host (murine leukocytes) and the malaria parasite suggests the plasmodium DNA is adequately removed from the host DNA.
Tags: Animal; Comparative Study
Descriptors: Chloroquine--antagonists and inhibitors--AI; *Chloroquine --pharmacology--PD; * **DNA** , Protozoan--genetics--GE; * **Plasmodium berghei** --genetics--GE; DNA, Protozoan--isolation and purification--IP; Drug Resistance--genetics--GE; Electrophoresis, Agar Gel--methods--MT; Malaria --parasitology--PS; Mice; Plasmodium berghei--drug effects--DE; Plasmodium berghei--isolation and purification--IP; Restriction Mapping
CAS Registry No.: 0 (DNA, Protozoan); 54-05-7 (Chloroquine)
Record Date Created: 19941103

15/9/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08142508 94277153 PMID: 8008025
Regular initiation of translation of Plasmodium berghei aldolase-2 after pre-mRNA splicing.
Certa U
Department PRTB, F. Hoffmann-La Roche Ltd., Basel, Switzerland.
Molecular and biochemical parasitology (NETHERLANDS) Feb 1994, 63 (2) p291-7, ISSN 0166-6851 Journal Code: 8006324

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

In Plasmodium falciparum aldolase a UAG or a regular AUG codon has been proposed for the initiation of ribosomal protein synthesis. A UAG codon present at the beginning of the coding sequence of the aldolase 2 gene (aldo-2) of Plasmodium berghei is not recognised in vitro as an initiation codon, which suggests addition of a regular AUG codon by mRNA splicing. Sequence analysis of cDNA amplified by the reversed polymerase chain reaction reveals addition of an ATG codon with a splice donor consensus sequence to the aldo-2 exon. By the same technique and northern blot analysis, substantial amounts of partially spliced P. berghei aldo-2 precursor mRNA are detected which could explain the isolation of immature P. falciparum aldolase cDNA clones starting with a stop codon.

Tags: Animal

Descriptors: Fructose-Bisphosphate Aldolase--genetics--GE; *Peptide Chain Initiation; * **Plasmodium berghei** --genetics--GE; * **RNA** Splicing; Base Sequence; Blotting, Northern; Cloning, Molecular; Codon; Consensus Sequence ; DNA, Complementary--genetics--GE; Exons--genetics--GE; Genes, Protozoan --genetics--GE; Genome; Molecular Sequence Data; Multigene Family--genetics --GE; Polymerase Chain Reaction; RNA Precursors--metabolism--ME; Sequence Analysis, DNA

Molecular Sequence Databank No.: GENBANK/M81793

CAS Registry No.: 0 (Codon); 0 (DNA, Complementary); 0 (RNA Precursors)

Enzyme No.: EC 4.1.2.13 (Fructose-Bisphosphate Aldolase)

Gene Symbol: aldo-2

Record Date Created: 19940721

15/9/11 (Item 11 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08082682 94222572 PMID: 8168966

Characterization and pathological significance of monoclonal DNA-binding antibodies from mice with experimental malaria infection.

Lloyd C M; Collins I; Belcher A J; Manuelpillai N; Wozencraft A O; Staines N A

Infection & Immunity Research Group,. King's College London, United Kingdom.

Infection and immunity (UNITED STATES) May 1994, 62 (5) p1982-8, ISSN 0019-9567 Journal Code: 0246127

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Malaria infection is accompanied by the production of a number of autoantibodies, including some that react with DNA. Epidemiological evidence implicates these in the nephritides that arise in human quartan malaria and in experimental malaria infections in mice. Through parallels with the involvement of DNA-reactive antibodies in the autoimmune syndrome systemic lupus erythematosus, a role for DNA-reactive antibodies in forming phlogistic immune deposits in the kidneys is implied. To more fully understand the relationship between antibodies of this specificity made in malaria and systemic lupus erythematosus, we prepared monoclonal DNA-reactive antibodies from BALB/c mice infected with Plasmodium berghei (clone RC) and compared their properties with those of other antibodies previously isolated from lupous MRL/Mp lpr/lpr and (NZB x NZW)F1 mice. Antibodies from malarial mice were all immunoglobulin M class and bound to single-stranded but not double-stranded DNA in an enzyme-linked immunosorbent assay. They also reacted with synthetic polyribonucleotides in the enzyme-linked immunosorbent assay and with parasitized erythrocytes and parasite pigment in kidney sections. None of the antibodies from lupous mice had identical specificities. The potential involvement of the DNA-reactive antibodies in malarial nephritis was demonstrated, by use of immunocytochemical methods, on the basis of their binding to existing

immune deposits in kidney sections from malarial mice, a similar property having been previously demonstrated for antibodies from lupous mice. Furthermore, antibodies from malarial mice expressed public idiotypes, notably Id.V-88, which is a member of the Id.16/6 family, commonly found on DNA-reactive antibodies in lupus and other infectious and connective tissue diseases. This study indicates that DNA-reactive antibodies in malaria have immunochemical properties similar but not identical to those of such antibodies in systemic lupus erythematosus and that they have the potential to participate in the formation of immune deposits in nephritic malarial kidneys.

Tags: Animal; Female; Support, Non-U.S. Gov't

Descriptors: Antibodies, Antinuclear--immunology--IM; *Antibodies, Monoclonal--immunology--IM; * **DNA** --immunology--IM; *Malaria--immunology --IM; * **Plasmodium berghei** --immunology--IM; Erythrocytes--parasitology--PS ; Immunoglobulin Idiotypes--analysis--AN; Kidney--immunology--IM; Lupus Erythematosus, Systemic--immunology--IM; Malaria--pathology--PA; Mice; Mice, Inbred BALB C

CAS Registry No.: 0 (Antibodies, Antinuclear); 0 (Antibodies, Monoclonal); 0 (Immunoglobulin Idiotypes); 9007-49-2 (DNA)

Record Date Created: 19940602

15/9/12 (Item 12 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

07981675 94142614 PMID: 1343732

Deletion, insertion and translocation of DNA sequences contribute to chromosome size polymorphism in Plasmodium berghei.

Janse C J; Mons B

Laboratory of Parasitology, University of Leiden, The Netherlands.

Memorias do Instituto Oswaldo Cruz (BRAZIL) 1992, 87 Suppl 3 p95-100, ISSN 0074-0276 Journal Code: 7502619

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Extensive chromosome size polymorphism arises in Plasmodium berghei during in vivo mitotic multiplication. Size differences between homologous chromosomes mainly involve rearrangements in the subtelomeric regions while internal chromosomal regions are more conserved. Size differences are almost exclusively due to differences in the copy number of a 2.3 kb subtelomeric repeat unit. Not only deletion of 2.3 kb repeats occurs, but addition of new copies of this repeat sometimes results in the formation of enlarged chromosomes. Even chromosomes which originally lack 2.3 kb repeats, can acquire these during mitotic multiplication. In one karyotype mutant, 2.3 kb repeats were inserted within one of the original telomeres of chromosome 4, creating an internal stretch of telomeric repeats. Chromosome translocation can contribute to chromosome size polymorphism as well. We found a karyotype mutant in which chromosome 7 with a size of about 1.4 Mb is translocated to chromosome 13/14 with a size of about 3 Mb, resulting in a rearranged chromosome, which was shown to contain a junction between internal DNA sequences of chromosome 13/14 and subtelomeric 2.3 kb repeats of chromosome 7. In this mutant a new chromosome of 1.4 Mb is present which consists of part of chromosome 13/14.

Tags: Animal; Support, Non-U.S. Gov't

Descriptors: Chromosomes--ultrastructure--UL; * **DNA** , Protozoan--genetics --GE; * **Plasmodium berghei** --genetics--GE; *Sequence Deletion; *Translocation (Genetics); Base Sequence; Crossing Over (Genetics); Gene Rearrangement; Mitosis; Molecular Sequence Data; Plasmodium berghei --ultrastructure--UL; Polymorphism (Genetics); Recombination, Genetic; Repetitive Sequences, Nucleic Acid

CAS Registry No.: 0 (DNA, Protozoan)

Record Date Created: 19940311

15/9/13 (Item 13 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

07913942 94051372 PMID: 8233621
Chromosomal polymorphism and sexual differentiation in Plasmodium.
Ponzi M; Alano P; Scotti R; Roca L
Laboratorio di Biologia Cellulare, Istituto Superiore di Sanita, Roma, Italia.
Parassitologia (ITALY) Jul 1993, 35 Suppl p87-9, ISSN 0048-2951 Journal Code: 0413724
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The correlation observed in several instances between the loss of ability to produce gametocytes and chromosomal rearrangements, prompted us to investigate in further detail the molecular bases of chromosomal polymorphism in Plasmodium. Generation of polymorphic karyotypes in Plasmodium involves important rearrangements, mostly occurring in subtelomeric position. Detailed analysis on the organisation of these regions have been carried out on the rodent malaria P. berghei and the human malaria P. falciparum. A 2.3kb sequence, tandemly organised in long clusters is shared by many P. berghei chromosomal ends. Variations in the copy number of this "module" account for most of the observed polymorphisms. In a P. falciparum cloned line (3D7) a common region spanning at least 40 kb, is present. It does not contain any repetitive structure other than the rep20 cluster, that appears to be completely contained within the common region. Notwithstanding the structural differences, human and rodent Plasmodia share the common feature of possessing long subtelomeric regions showing, thus, a homology between the different chromosomes.
Tags: Animal; Comparative Study; Female; Male
Descriptors: *Chromosomes--ultrastructure--UL; *Plasmodium berghei --genetics--GE; *Plasmodium falciparum--genetics--GE; *Polymorphism (Genetics); Chromosome Aberrations; Chromosome Deletion; Chromosome Mapping ; **DNA** , Protozoan--genetics--GE; **Plasmodium berghei** --physiology--PH; Plasmodium falciparum--physiology--PH; Repetitive Sequences, Nucleic Acid; Species Specificity
CAS Registry No.: 0 (DNA, Protozoan)
Record Date Created: 19931216

15/9/14 (Item 14 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07913930 94051360 PMID: 8233609
Mobile repeat units in Plasmodium berghei.
Dore E; Frontali C; Pace T
Istituto Superiore di Sanita, Roma, Italy.
Parassitologia (ITALY) Jul 1993, 35 Suppl p39-42, ISSN 0048-2951 Journal Code: 0413724
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Tags: Animal; Support, Non-U.S. Gov't
Descriptors: **DNA** , Protozoan--genetics--GE; * **Plasmodium berghei** --genetics--GE; *Repetitive Sequences, **Nucleic** Acid; Base Sequence; Karyotyping; Mice; Molecular Sequence Data
CAS Registry No.: 0 (DNA, Protozoan)
Record Date Created: 19931216

15/9/15 (Item 15 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07702323 93228187 PMID: 8470780
Differentiation of Toxoplasma gondii from closely related coccidia by riboprint analysis and a surface antigen gene polymerase chain reaction.
Brindley P J; Gazzinelli R T; Denkers E Y; Davis S W; Dubey J P; Belfort

R; Martins M C; Silveira C; Jamra L; Waters A P; et al
Laboratory of Parasitic Diseases, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland.
American journal of tropical medicine and hygiene (UNITED STATES) Mar 1993, 48 (3) p447-56, ISSN 0002-9637 Journal Code: 0370507
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: AIM; INDEX MEDICUS

The tachyzoite of the human pathogen Toxoplasma gondii is morphologically indistinguishable from the proliferative stages of some other zoonotic coccidia, including Sarcocystis. To determine the identity of such coccidia obtained from human tissues and other sources, we compared riboprints (through restriction enzyme analysis of the polymerase chain reaction [PCR]-amplified small subunit rRNA gene) of the following protozoa: the RH and ts-4 strains of T. gondii, lines OH3 and S11, which are two recently isolated T. gondii-like parasites from Brazil, Neospora caninum, Sarcocystis species, and the malarial parasite Plasmodium berghei. In addition, the protozoan genomes were examined by PCR for homologs of surface antigen genes of T. gondii, and by Southern hybridization to the heterologous rRNA gene probe pSM 389. Strains OH3, S11, ts-4, and RH shared identical riboprints, and OH3, S11, and ts-4 have p22 and p30 surface antigen gene structures similar to RH. In contrast, riboprints for N. caninum and T. gondii differ with respect to Dde 1 sites, and moreover, their genomes vary significantly from one another at both the p22 and p30 gene loci. The riboprints of Sarcocystis and P. berghei differ markedly from T. gondii and N. caninum and from each other. Bam HI pSM 389 restriction fragment length polymorphisms differentiate ts-4 from RH, OH3, and S11. Our results confirm that OH3 and S11 are indeed T. gondii, but that N. caninum and T. gondii are likely to be separate species, thereby resolving previous uncertainties concerning the identity of these parasites. Together, the variation in riboprints and surface antigen gene structure reflects the phylogenetic diversity among these coccidia, and in addition, confirms the value of riboprinting in the identification of apicomplexan parasites such as T. gondii.

Tags: Animal; Comparative Study; Human; Support, U.S. Gov't, P.H.S.
Descriptors: *Antigens, Protozoan--genetics--GE; *RNA, Protozoan --genetics--GE; *RNA, Ribosomal--genetics--GE; *Toxoplasma--isolation and purification--IP; Antigens, Surface--genetics--GE; Apicomplexa--genetics --GE; Apicomplexa--immunology--IM; Apicomplexa --isolation and purification--IP; Base Sequence; Blotting, Southern; DNA, Protozoan --analysis--AN; DNA, Protozoan--chemistry--CH; DNA, Ribosomal--analysis --AN; DNA, Ribosomal--chemistry--CH; Molecular Sequence Data; **Nucleic Acid Hybridization** ; **Plasmodium** berghei--genetics--GE; **Plasmodium berghei** --immunology--IM; Plasmodium berghei--isolation and purification --IP; Polymerase Chain Reaction; Restriction Mapping; Sarcocystis--genetics --GE; Sarcocystis--immunology--IM; Sarcocystis --isolation and purification--IP; Swine; Toxoplasma--genetics--GE; Toxoplasma--immunology --IM
CAS Registry No.: 0 (Antigens, Protozoan); 0 (Antigens, Surface); 0 (DNA, Protozoan); 0 (DNA, Ribosomal); 0 (RNA, Protozoan); 0 (RNA, Ribosomal)
Record Date Created: 19930510

15/9/16 (Item 16 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07570887 93096513 PMID: 1461677
Assessment of parasite population dynamics in mixed infections of rodent plasmodia.
Snounou G; Bourne T; Jarra W; Viriyakosol S; Wood J C; Brown K N
Division of Parasitology, National Institute for Medical Research, The Ridgeway, Mill Hill, London.
Parasitology (ENGLAND) Dec 1992, 105 (Pt 3) p363-74, ISSN 0031-1820 Journal Code: 0401121
Document type: Journal Article
Languages: ENGLISH

Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Cloned lines of the four rodent Plasmodium species can be differentiated by the RFLP pattern generated following Southern blotting and probing with PCsv4.1, a probe derived from a P. chabaudi chabaudi genomic library. Groups of CBA/Ca mice were inoculated simultaneously with cloned lines from two parasite species or strains. Six mixed species and three mixed strain infections using rodent malaria lines were initiated. The composition of the parasite population in each group was determined qualitatively and semi-quantitatively by analysis of the DNA purified from daily blood samples, thereby providing a dynamic representation of each mixed infection. Effects on the course of parasitaemias are presented and discussed.

Tags: Animal; Male

Descriptors: *Malaria--parasitology--PS; *Plasmodium --growth and development--GD; *Plasmodium berghei--growth and development--GD; *Plasmodium chabaudi--growth and development--GD; *Plasmodium yoelii --growth and development--GD; Blotting, Southern; DNA Probes; DNA, Protozoan--blood--BL; Erythrocytes--parasitology--PS; Malaria--blood--BL; Mice; Mice, Inbred CBA; **Nucleic** Acid **Hybridization** ; Plasmodium --genetics--GE; **Plasmodium berghei** --genetics--GE; Plasmodium chabaudi --genetics--GE; Plasmodium yoelii--genetics--GE

CAS Registry No.: 0 (DNA Probes); 0 (DNA, Protozoan)

Record Date Created: 19930114

15/9/17 (Item 17 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

07539562 93064842 PMID: 1359498

Identification and quantification of rodent malaria strains and species using gene probes.

Snounou G; Bourne T; Jarra W; Viriyakosol S; Brown K N

Division of Parasitology, National Institute for Medical Research, Mill Hill, London.

Parasitology (ENGLAND) Aug 1992, 105 (Pt 1) p21-7, ISSN 0031-1820 Journal Code: 0401121

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A DNA probe PCsv4 and a subclone thereof PCsv4.1, hybridize specifically to rodent malaria DNA. DNA purified from a small volume (10 microliters) of infected mouse blood was used to determine the composition of the parasite population present. The hybridization signal following PCsv4 probing of slot-blotted DNA correlated directly with parasitaemia. The hybridization pattern and intensity, resulting from probing restriction enzyme digested and Southern-blotted genomic DNA, determined the identity of the infecting parasite line(s), and provided a semi-quantitative measure of parasite burden. Fifteen parasite lines representative of all four Plasmodium species infecting rodents can be differentiated in this way.

Tags: Animal; Male

Descriptors: *DNA Probes; *DNA, Protozoan--analysis--AN; *Malaria --parasitology--PS; *Plasmodium--classification--CL; Autoradiography; Blotting, Southern; Deoxyribonuclease EcoRI; Disease Models, Animal; Mice; Mice, Inbred CBA; **Nucleic** Acid **Hybridization** ; Plasmodium--genetics--GE; **Plasmodium berghei** --classification--CL; Plasmodium berghei--genetics--GE ; Plasmodium chabaudi--classification--CL; Plasmodium chabaudi--genetics --GE; Plasmodium yoelii--classification--CL; Plasmodium yoelii--genetics --GE; Polymorphism, Restriction Fragment Length; Regression Analysis; Restriction Mapping

CAS Registry No.: 0 (DNA Probes); 0 (DNA, Protozoan)

Enzyme No.: EC 3.1.21.- (Deoxyribonuclease EcoRI)

Record Date Created: 19921214

15/9/21 (Item 21 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

07216701 92160616 PMID: 1789198
Nucleotide status in erythrocytes of rats infected with Plasmodium berghei.
Jacobasch G; Werner A; Siems W; Gerth C
Institute of Biochemistry, Medical Faculty, Humboldt University, Berlin, F.R.G.
Advances in experimental medicine and biology (UNITED STATES) 1991, 309A p161-4, ISSN 0065-2598 Journal Code: 0121103
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Tags: Animal
Descriptors: Adenosine--blood--BL; *Erythrocytes--metabolism--ME; *Hypoxanthines--blood--BL; *Inosine--blood--BL; *Malaria--blood--BL; * **Plasmodium berghei** ; *Purine **Nucleotides** --metabolism--ME; Adenine Nucleotides--blood--BL; Guanine Nucleotides--blood--BL; Hemolysis; Hypoxanthine; Rats; Uracil Nucleotides--blood--BL
CAS Registry No.: 0 (Adenine Nucleotides); 0 (Guanine Nucleotides); 0 (Hypoxanthines); 0 (Purine Nucleotides); 0 (Uracil Nucleotides); 58-61-7 (Adenosine); 58-63-9 (Inosine); 68-94-0 (Hypoxanthine)
Record Date Created: 19920323

15/9/28 (Item 28 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06651675 90351430 PMID: 2201292
Nucleotide status in erythrocytes of rats infected with Pl. berghei.
Werner A; Jacobasch G; Siems W; Gerth C; Schreiter C
Institute of Biochemistry, Humboldt University, Berlin, GDR.
Biomedica biochimica acta (GERMANY, EAST) 1990, 49 (2-3) pS301-4, ISSN 0232-766X Journal Code: 8304435
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Nucleotide concentrations in erythrocytes of rats infected with Plasmodium berghei were measured by ion-pair reversed-phase HPLC. UTP and GTP levels were higher in highly infected red blood cells obtained after density separation. The infected red blood cells possess higher hypoxanthine, adenine, and adenosine levels.
Tags: Animal
Descriptors: Erythrocytes--metabolism--ME; * **Nucleotides** --metabolism--ME ; * **Plasmodium berghei** --metabolism--ME; Centrifugation, Density Gradient; Chromatography, High Pressure Liquid; Erythrocytes--parasitology--PS; Rats
CAS Registry No.: 0 (Nucleotides)
Record Date Created: 19900917

15/9/30 (Item 30 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06580431 90277415 PMID: 2190950
Detection of DNA sequences in Plasmodium berghei by means of in situ hybridization.
Obst M; Cornelissen A W
Max-Planck-Institut fur Biologie, Molecular Parasitology Unit, Tubingen, Federal Republic of Germany.
Histochemistry (GERMANY, WEST) 1990, 94 (1) p101-7, ISSN 0301-5564 Journal Code: 0411300
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Subfile: INDEX MEDICUS
A non-radioactive in situ hybridization technique, used to map unique DNA sequences to plant chromosomes, has been adapted for the localization of specific DNA sequences in nuclei of Plasmodium berghei. After hybridization using probes labeled with biotin-11-dUTP, the formed DNA/DNA hybrids were detected by fluorescence microscopy using a specific double-layer antibody technique. Besides its high resolution, this procedure is characterized by a high sensitivity, allowing the detection of a unique sequence as small as 2.5 kb.
Tags: Animal; Support, Non-U.S. Gov't
Descriptors: DNA--analysis--AN; * **DNA Probes** ; *Nucleic Acid **Hybridization** ; * **Plasmodium** berghei--genetics--GE; Biotin; Cell Nucleus --analysis--AN; Immunohistochemistry
CAS Registry No.: 0 (DNA Probes); 58-85-5 (Biotin); 9007-49-2 (DNA)
Record Date Created: 19900718

15/9/29 (Item 29 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06649590 90348721 PMID: 1974695
Generation of chromosome size polymorphism during in vivo mitotic multiplication of Plasmodium berghei involves both loss and addition of subtelomeric repeat sequences.
Ponzi M; Janse C J; Dore E; Scotti R; Pace T; Reterink T J; van der Berg F M; Mons B
Laboratorio di Biologia Cellulare, Istituto Superiore di Sanita, Rome, Italy.
Molecular and biochemical parasitology (NETHERLANDS) Jun 1990, 41 (1) p73-82, ISSN 0166-6851 Journal Code: 8006324
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Extensive chromosome size polymorphism arises in Plasmodium berghei during in vivo mitotic multiplication. Size differences between homologous chromosomes involve rearrangements occurring in the subtelomeric portions while internal chromosomal regions do not contribute significantly to chromosome size polymorphism. Differences in the copy number of a 2.3-kb subtelomeric repeated unit are shown to correlate with size variations, and in at least one case to account completely for the size difference between two variants of the same chromosome.
Tags: Animal; Support, Non-U.S. Gov't
Descriptors: *Chromosomes; *Mitosis; *Plasmodium berghei--genetics--GE; *Polymorphism, Restriction Fragment Length; *Repetitive Sequences, Nucleic Acid; Blotting, Southern; Flow Cytometry; Karyotyping; **Nucleic** Acid **Hybridization** ; **Plasmodium** berghei--cytology--CY
Record Date Created: 19900917

15/9/31 (Item 31 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06521490 90220630 PMID: 2183034
Organization of subtelomeric repeats in Plasmodium berghei.
Dore E; Pace T; Ponzi M; Picci L; Frontali C
Laboratory of Cell Biology, Istituto Superiore di Sanita, Rome, Italy.
Molecular and cellular biology (UNITED STATES) May 1990, 10 (5) p2423-7, ISSN 0270-7306 Journal Code: 8109087
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Several (but not all) Plasmodium berghei chromosomes bear in the subtelomeric position a cluster of 2.3-kilobase (kb) tandem repeats. The 2.3-kb unit contains 160 base pairs of telomeric sequence. The resulting subtelomeric structure is one in which stretches of telomeric sequences are

periodically spaced by a 2.1-kb reiterated sequence. This periodic organization of internal telomeric sequences might be related to chromosome-size polymorphisms involving the loss or addition of subtelomeric 2.3-kb units.
Tags: Animal; Support, Non-U.S. Gov't
Descriptors: Chromosomes--ultrastructure--UL; * **Plasmodium berghei** --genetics--GE; *Repetitive Sequences, **Nucleic** Acid; Base Sequence; Chromosome Mapping; Electrophoresis, Agar Gel; Molecular Sequence Data; Restriction Mapping
Molecular Sequence Databank No.: GENBANK/M34601; GENBANK/M34602
Record Date Created: 19900521

15/9/36 (Item 36 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06113411 89196577 PMID: 2649389
Plasmodium berghei: gametocyte production, DNA content, and chromosome-size polymorphisms during asexual multiplication in vivo.
Janse C J; Boorsma E G; Ramesar J; van Vianen P; van der Meer R; Zenobi P ; Casaglia O; Mons B; van der Berg F M
Laboratory of Parasitology, University of Leiden, The Netherlands.
Experimental parasitology (UNITED STATES) Apr 1989, 68 (3) p274-82, ISSN 0014-4894 Journal Code: 0370713
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
In this study the DNA content and the karyotype of clones of Plasmodium berghei, which differed in the capability to produce gametocytes, were determined. The DNA content per haploid genome was established by cytofluorometric methods after staining of the haploid merozoites with DNA-specific fluorescent dyes. Field inversion gel electrophoresis was used to establish the number and size of the chromosomes. Parasites of a high gametocyte producer clone (original HP) and a low producer clone (original LP) contained 13 to 14 chromosomes in the size range of 0.5-3.8 megabase. In four independent experiments parasites of the original HP clone were maintained in mice and were mechanically transmitted for prolonged periods of time (up to 90 weeks). During the transmission period the capability to produce gametocytes decreased in all four lines. After mosquito transmission of parasites from these low producer lines, the gametocyte production returned to the level of the original HP clone. The total DNA content per haploid genome of low producer parasites was not significantly different from that of HP parasites. During prolonged periods of asexual multiplication of the HP clone in vivo, changes in the relative size of several chromosomes were detected. Mosquito transmission of the original HP clone did not result in a change of the karyotype. However, novel karyotypes were readily observed after mosquito transmission of parasites of the low producer lines. The decrease of the capability to produce gametocytes did not necessarily involve detectable changes in DNA content or in karyotype.
Tags: Animal; Support, Non-U.S. Gov't
Descriptors: Anopheles--parasitology--PS; * **DNA** --analysis--AN; * **Plasmodium berghei** --growth and development--GD; *Polymorphism (Genetics) ; Electrophoresis, Agar Gel; Flow Cytometry; Karyotyping; Mice; Plasmodium berghei--genetics--GE; Rats; Rats, Inbred Strains
CAS Registry No.: 9007-49-2 (DNA)
Record Date Created: 19890518

15/9/37 (Item 37 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05809368 88232803 PMID: 2836731
Primary sequences of two small subunit ribosomal RNA genes from Plasmodium falciparum.
McCutchan T F; de la Cruz V F; Lal A A; Gunderson J H; Elwood H J; Sogin M L

Laboratory of Parasitic Diseases, National Institute of Allergy and Infectious Diseases, Bethesda, MD.
Molecular and biochemical parasitology (NETHERLANDS) Feb 1988, 28 (1) p63-8, ISSN 0166-6851 Journal Code: 8006324
Contract/Grant No.: 6M32964; PHS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

We have determined the complete sequence of two structurally distinct 18S ribosomal RNA genes from the malarial parasite Plasmodium falciparum. S1 nuclease analyses demonstrate that only one of the genes is represented in stable rRNA populations isolated from blood-stage parasites. Comparisons of homologous rRNA genes from Plasmodium berghei and P. falciparum reveal that they are identical at 86% of their positions. From comparisons of the Plasmodium genes to that of humans, it was possible to design genus-specific as well as species-specific oligonucleotide probes that can be used to distinguish the parasite 18S ribosomal RNA from that of its host. The utilization of these probes as diagnostic reagents is discussed.

Tags: Animal; Comparative Study; Human; Support, U.S. Gov't, P.H.S.

Descriptors: *Genes; *Plasmodium falciparum--genetics--GE; *RNA, Ribosomal--genetics--GE; *RNA, Ribosomal, 18S--genetics--GE; Aspergillus Nuclease S1; Base Sequence; Endonucleases; Molecular Sequence Data; Nucleic Acid **Hybridization** ; Oligonucleotides--genetics--GE; Plasmids; **Plasmodium berghei** --genetics--GE; Species Specificity; Transcription, Genetic

Molecular Sequence Databank No.: GENBANK/M19172; GENBANK/M19173

CAS Registry No.: 0 (Oligonucleotides); 0 (Plasmids); 0 (RNA, Ribosomal); 0 (RNA, Ribosomal, 18S)

Enzyme No.: EC 3.1.- (Endonucleases); EC 3.1.30.1 (Aspergillus Nuclease S1)

Record Date Created: 19880712

15/9/38 (Item 38 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05563237 87315195 PMID: 3041211

Telomeric motifs are present in a highly repetitive element in the Plasmodium berghei genome.

Pace T; Ponzi M; Dore E; Frontali C
Molecular and biochemical parasitology (NETHERLANDS) Jun 1987, 24 (2) p193-202, ISSN 0166-6851 Journal Code: 8006324
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Using as probes the subfragments of the telomeric sequence previously cloned by us from Plasmodium berghei DNA, we identified and cloned a 2.3 kb repeat, largely overlapping the original telomeric insert. Restriction mapping indicated that cloned inserts (2.3 kb in length) represented circularly permutated versions of a rather well conserved repeated element, at least in part organized in tandem. The 2.3 kb repeat family with a copy number of about 300 occupies about 4% of the whole genome. The copies are unevenly distributed among the chromosome-sized molecules revealed by pulsed field gradient electrophoresis. Complete sequence determination of the 2.3 kb element revealed that telomere-related motifs are present with a characteristic pattern in a set of tandem repeats, 27 bp long. The perfect conservation of these motifs as well as the pattern of chromosomal distribution suggest that we are dealing with a specialised structure subject to selective mechanisms of amplification and maintenance.

Tags: Animal; Support, Non-U.S. Gov't

Descriptors: **DNA** --analysis--AN; *Genes; * **Plasmodium berghei** --genetics --GE; *Repetitive Sequences, **Nucleic** Acid; Base Sequence; Chromosome Mapping; Cloning, Molecular; DNA Restriction Enzymes; Electrophoresis, Agar Gel; Nucleic Acid Hybridization; Sequence Homology, Nucleic Acid

Molecular Sequence Databank No.: GENBANK/M19300

CAS Registry No.: 9007-49-2 (DNA)

Enzyme No.: EC 3.1.21 (DNA Restriction Enzymes)
Record Date Created: 19871020

15/9/41 (Item 41 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05448986 87201679 PMID: 3033497
Tandemly arranged gene clusters of malarial parasites that are highly conserved and transcribed.
Vaidya A B; Arasu P
Molecular and biochemical parasitology (NETHERLANDS) Jan 15 1987, 22 (2-3) p249-57, ISSN 0166-6851 Journal Code: 8006324
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
A molecular clone containing a 5.8 kb Eco RI fragment was isolated from a genomic library of the rodent malarial parasite Plasmodium yoelii. The P. yoelii genome contains about 150 copies of this sequence, making up almost 3% of the DNA. These sequences are tandemly arrayed in head-to-tail configurations with the unit length of the repeat being 5.8 kb. Several poly(A+) RNAs of P. yoelii ranging from 1.6 to 0.3 kb are recognized by the 5.8 kb clone. Five additional species of malarial parasites (P. chabaudi, P. berghei, P. falciparum, P. knowlesi, and P. cynomolgi) contain tandemly repeated arrays of sequences having the same unit length of 5.8 kb, which readily hybridize to the sequence cloned from P. yoelii.
Tags: Animal; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.
Descriptors: *DNA--analysis--AN; *Genes; *Plasmodium--genetics--GE; Cloning, Molecular; DNA--genetics--GE; DNA Restriction Enzymes; Deoxyribonuclease EcoRI; Electrophoresis, Agar Gel; Mice; **Nucleic** Acid **Hybridization** ; **Plasmodium** berghei--genetics--GE; Plasmodium falciparum --genetics--GE; Repetitive Sequences, Nucleic Acid; Transcription, Genetic; Translation, Genetic
CAS Registry No.: 9007-49-2 (DNA)
Enzyme No.: EC 3.1.21 (DNA Restriction Enzymes); EC 3.1.21.- (Deoxyribonuclease EcoRI)
Record Date Created: 19870526

15/9/42 (Item 42 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05332941 87086558 PMID: 3540280
Sequence of the small subunit ribosomal RNA gene expressed in the bloodstream stages of Plasmodium berghei: evolutionary implications.
Gunderson J H; McCutchan T F; Sogin M L
Journal of protozoology (UNITED STATES) Nov 1986, 33 (4) p525-9, ISSN 0022-3921 Journal Code: 2985197R
Contract/Grant No.: GM32964; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
We have determined the complete nucleotide sequence of the coding region of the small subunit rRNA gene expressed by bloodstream stages of the apicomplexan Plasmodium berghei. It is 2059 nucleotides long. Elements contributing to its relatively large size are all concentrated in regions known to be variable in length among eukaryotes. In a phylogenetic tree constructed from pairwise comparisons of eukaryotic small subunit rRNA sequences, the apicomplexan line branches at a rather early point in eukaryotic evolution before any multicellular kingdoms had yet appeared.
Tags: Animal; Comparative Study; Support, U.S. Gov't, P.H.S.
Descriptors: Genes; * **Plasmodium berghei** --genetics--GE; * **RNA** , Ribosomal--genetics--GE; Base Sequence; Evolution; Phylogeny
Molecular Sequence Databank No.: GENBANK/M14599
CAS Registry No.: 0 (RNA, Ribosomal)

Record Date Created: 19870205

15/9/45 (Item 45 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05237157 86311078 PMID: 3092048
DNA synthesis in Plasmodium berghei during asexual and sexual development.
Janse C J; van der Klooster P F; van der Kaay H J; van der Ploeg M; Overdulve J P
Molecular and biochemical parasitology (NETHERLANDS) Aug 1986, 20 (2) p173-82, ISSN 0166-6851 Journal Code: 8006324
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
DNA contents of individual stages of Plasmodium berghei were measured by direct microfluorometry after Feulgen-pararosaniline (SO2) staining. Sporozoites, intra-erythrocytic ringforms and trophozoites (until at least 15 h after invasion) are haploid and non-synthesizing DNA. DNA is synthesized just before and during schizogony, which takes 4-6 h. Genome duplication and segregation are alternating events throughout this process. Mature micro- and macrogametocytes have DNA contents between the haploid and diploid value; most, if not all of the DNA in excess of the haploid value is synthesized during the last 5-10 h of maturation. During gametogenesis microgametocytes within 8-10 min synthesize DNA steadily and at a very high rate to more than the octoploid value while the DNA content of macrogametocytes remains constant. Fertilization in vitro takes place within 1 h after gamete formation. Within 2 h and coinciding with the onset of meiosis the zygote then synthesizes DNA up to almost the tetraploid value, after which synthesis stops during ookinete development. All the above mentioned processes of DNA synthesis are reversibly inhibited by aphidicolin (C50 from 3-13 microM). From the rate of DNA synthesis during microgametogenesis we calculated a minimum of 1300 origins of replication in the haploid genome of P. berghei.
Tags: Animal; Support, Non-U.S. Gov't
Descriptors: **DNA** --biosynthesis--BI; * **Plasmodium berghei** --genetics--GE ; Aphidicolin; Cytophotometry; Diploidy; Diterpenes--pharmacology--PD; Gametogenesis; Genes; Haploidy; Plasmodium berghei--growth and development --GD; Plasmodium berghei--physiology--PH; Rats; Reproduction; Reproduction, Asexual
CAS Registry No.: 0 (Diterpenes); 38966-21-1 (Aphidicolin); 9007-49-2 (DNA)
Record Date Created: 19861023

15/9/46 (Item 46 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05186251 86262691 PMID: 3088783
Rapid repeated DNA replication during microgametogenesis and DNA synthesis in young zygotes of Plasmodium berghei.
Janse C J; Van der Klooster P F; Van der Kaay H J; Van der Ploeg M; Overdulve J P
Transactions of the Royal Society of Tropical Medicine and Hygiene (ENGLAND) 1986, 80 (1) p154-7, ISSN 0035-9203 Journal Code: 7506129
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Tags: Support, Non-U.S. Gov't
Descriptors: **DNA** --biosynthesis--BI; * **DNA** Replication; * **Plasmodium berghei** --metabolism--ME; Aphidicolin; DNA Polymerase II--antagonists and inhibitors--AI; DNA Replication--drug effects--DE; Diterpenes--pharmacology --PD; Gametogenesis; Mitomycin; Mitomycins--pharmacology--PD; Plasmodium berghei--genetics--GE; Zygote--metabolism--ME

CAS Registry No.: 0 (Diterpenes); 0 (Mitomycins); 38966-21-1 (Aphidicolin); 50-07-7 (Mitomycin); 9007-49-2 (DNA)
Enzyme No.: EC 2.7.7.- (DNA Polymerase II)
Record Date Created: 19860725

15/9/47 (Item 47 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05182674 86257278 PMID: 3523238
Infectivity of Plasmodium berghei sporozoites measured with a DNA probe.
Ferreira A; Enea V; Morimoto T; Nussenzweig V
Molecular and biochemical parasitology (NETHERLANDS) May 1986, 19 (2) p103-9, ISSN 0166-6851 Journal Code: 8006324
Contract/Grant No.: AHRAI21642-01; AH; BHP
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
A 2.3 kb, 32P-labeled repetitive DNA probe of Plasmodium berghei was used to measure the amount of parasite DNA in the liver of Norway Brown rats and mice infected with sporozoites. Standard hybridization curves were obtained by probing different amounts (100 pg to 1 microgram) of P. berghei DNA immobilized on nitrocellulose filters. Host DNA did not interfere with hybridization specificity and sensitivity. A 100-fold increase in hepatic parasite DNA was detected between 25 h post-infection and the peak of parasite proliferation, detected at 44 h. The amount of parasite DNA increased with the number of injected sporozoites. At 5 h post-infection, a large proportion of parasite DNA was found in the spleen. However, this diminished with time and was negligible in amount at 25 h. A significant number of viable sporozoites were probably cleared in the spleen, since considerably more parasite DNA was found in the livers of splenectomized rats than in sham-operated counterparts. Although older rats develop much lower parasitemias upon inoculation of sporozoites, no significant differences were observed in the amount of parasite DNA in rats, 43 and 152 days old, injected with equal numbers of sporozoites. The higher resistance to malaria displayed by older rats is probably controlled by post-hepatic events. The infectivity of sporozoites for A/J mice was calculated to be about 1/20th that of Norway Brown rats.
Tags: Animal; Female; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.
Descriptors: *DNA--analysis--AN; *Liver--parasitology--PS; *Malaria --parasitology--PS; *Plasmodium berghei--genetics--GE; Aging; Mice; Mice, Inbred A; **Nucleic** Acid **Hybridization** ; **Plasmodium** berghei--growth and development--GD; Plasmodium berghei--pathogenicity--PY; Rats; Rats, Inbred BN; Spleen--parasitology--PS
CAS Registry No.: 9007-49-2 (DNA)
Record Date Created: 19860801

15/9/48 (Item 48 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05135122 86213484 PMID: 2423000
Cytofluorimetric analysis of DNA content in different life stages of Plasmodium yoelii.
Casaglia O; Dore E; Frontali C; Ramoni C; Zenobi P
Annali dell'Istituto superiore di sanita (ITALY) 1985, 21 (3) p401-6 , ISSN 0021-2571 Journal Code: 7502520
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Tags: Animal; Comparative Study; Support, Non-U.S. Gov't
Descriptors: **DNA** --analysis--AN; * **Plasmodium berghei** --analysis--AN; Anopheles--parasitology--PS; Erythrocytes--parasitology--PS; Ethidium --diagnostic use--DU; Fluorescence; Mice; Plasmodium berghei--growth and

development--GD; Plasmodium berghei--isolation and purification--IP; Plicamycin--diagnostic use--DU; Staining and Labeling
CAS Registry No.: 18378-89-7 (Plicamycin); 3546-21-2 (Ethidium); 9007-49-2 (DNA)
Record Date Created: 19860606

15/9/49 (Item 49 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05101286 86167268 PMID: 3514510
The ribosomal genes of Plasmodium.
McCutchan T F
International review of cytology (UNITED STATES) 1986, 99 p295-309, ISSN 0074-7696 Journal Code: 2985180R
Document type: Journal Article; Review
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
(40 Refs.)
Tags: Animal
Descriptors: **DNA** , Ribosomal--genetics--GE; *Genes, Structural; * **Plasmodium berghei** --genetics--GE; Base Sequence; Haploidy; Phenotype; Plasmodium berghei--growth and development--GD
CAS Registry No.: 0 (DNA, Ribosomal)
Record Date Created: 19860515

15/9/59 (Item 59 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

04218200 83213442 PMID: 6304071
The four ribosomal DNA units of the malaria parasite Plasmodium berghei. Identification, restriction map, and copy number analysis.
Dame J B; McCutchan T F
Journal of biological chemistry (UNITED STATES) Jun 10 1983, 258 (11) p6984-90, ISSN 0021-9258 Journal Code: 2985121R
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The four ribosomal RNA genes (rDNA units) of the rodent malaria parasite, Plasmodium berghei, were identified and mapped by restriction enzyme analysis and Southern blot hybridization of genomic DNA. Although the four genes share common characteristics, they appear to be internally different from each other in expanse and sequence. One HindIII site near the 3' end of the coding region for the large rRNA is the only restriction site which we have detected that is conserved in all of the genes. The distance between the conserved HindIII site and the coding region for the small rRNA is at least 1-2 kilobases longer in two of the rDNA units than in a third unit. None of the four rDNA units were linked by restriction mapping where about 150 kilobases of the genome were accounted for. The copy number of two of the rDNA units was determined to be approximately 1 per haploid genome by quantitative analysis of cloned (plasmid) DNA versus genomic DNA digests on Southern blots. The other two genes also appear to be present in 1 copy. Restriction analysis confirms both the low copy number and that these genes are not in an easily recognizable tandem array. The low number of rDNA units requires that new copies of the genome produced during intraerythrocytic growth be active in RNA synthesis soon after their replication.
Tags: Animal
Descriptors: **DNA** --genetics--GE; *Genes, Structural; * **Plasmodium berghei** --genetics--GE; Base Sequence; DNA--isolation and purification--IP; DNA Restriction Enzymes; DNA, Ribosomal; Gene Amplification; Nucleic Acid Hybridization
CAS Registry No.: 0 (DNA, Ribosomal); 9007-49-2 (DNA)
Enzyme No.: EC 3.1.21 (DNA Restriction Enzymes)

Record Date Created: 19830715

15/9/65 (Item 65 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03085385 79157626 PMID: 372893
The ribosomes of Plasmodium berghei: isolation and ribosomal ribonucleic acid analysis.
Miller F W; Ilan J
Parasitology (ENGLAND) Dec 1978, 77 (3) p345-65, ISSN 0031-1820 Journal Code: 0401121
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Ribosomes and high molecular weight ribosomal ribonucleic acid (rRNA) from the blood stages of Plasmodium berghei parasites were studied in preparations free from host ribosome contamination. Purified malarial ribosomes were isolated in high yield from a population of ultrastructurally intact, viable parasites by hypertonic lysis with Triton X-100 and differential centrifugation. These ribosomes were shown to be derived from active polysomes and could be dissociated into subunits by puromycin-0.5 M KCl treatment. Malarial rRNA extracted from purified 40S and 60S ribosomal subunits was characterized by electrophoretic, sedimentation and base ratio analyses. Like certain other protozoa, the P. berghei 40S ribosomal subunit possessed an exceptionally large RNA species (mol. wt 0.9 X 10(6), while RNA isolated from the parasite's 60S subunit (mol. wt 1.5 X 10(6)) was specifically 'nicked' to produce one large component (mol.wt 1.2 X 10(6)) and one small component (mol.wt 0.3 X 10(6)) in equimolar quantities. These rRNA's migrate identically on polyacrylamide gels after heating to 63 degrees C for 5 min or under denaturing conditions in the presence of formamide, indicating an absence of aggregation and non-specific degradation of the rRNA species. Base composition studies showed P. berghei rRNA to be low in guanosine and cytosine content, as is the case for protozoa generally.
Tags: Animal; Female
Descriptors: **Plasmodium berghei** --analysis--AN; * **RNA** , Ribosomal --analysis--AN; *Ribosomes--analysis--AN; Base Sequence; Electrophoresis, Polyacrylamide Gel; Mice; Molecular Weight; RNA, Ribosomal--isolation and purification--IP; Ultracentrifugation
CAS Registry No.: 0 (RNA, Ribosomal)
Record Date Created: 19790611
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      $0.01  Estimated cost File467
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      $8.74  Estimated cost this search
      $8.74  Estimated total session cost   0.576 DialUnits


### Status: Signed Off. (1 minutes)
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Primary sequences of two small subunit ribosomal RNA genes from Plasmodium falciparum.

McCutchan T F; de la Cruz V F; Lal A A; Gunderson J H; Elwood H J; Sogin M L

Laboratory of Parasitic Diseases, National Institute of Allergy and Infectious Diseases, Bethesda, MD.

Molecular and biochemical parasitology (NETHERLANDS) Feb 1988, 28 (1) p63-8, ISSN 0166-6851 Journal Code: 8006324

Contract/Grant No.: 6M32964; PHS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

We have determined the complete sequence of two structurally distinct 18S ribosomal RNA genes from the malarial parasite Plasmodium falciparum. S1 nuclease analyses demonstrate that only one of the genes is represented in stable rRNA populations isolated from blood-stage parasites. Comparisons of homologous rRNA genes from Plasmodium berghei and P. falciparum reveal that they are identical at 86% of their positions. From comparisons of the Plasmodium genes to that of humans, it was possible to design genus-specific as well as species-specific oligonucleotide probes that can be used to distinguish the parasite 18S ribosomal RNA from that of its host. The utilization of these probes as diagnostic reagents is discussed.

Tags: Animal; Comparative Study; Human; Support, U.S. Gov't, P.H.S.

Descriptors: *Genes; *Plasmodium falciparum--genetics--GE; *RNA, Ribosomal--genetics--GE; *RNA, Ribosomal, 18S--genetics--GE; Aspergillus Nuclease S1; Base Sequence; Endonucleases; Molecular Sequence Data; Nucleic Acid **Hybridization** ; Oligonucleotides--genetics--GE; Plasmids; **Plasmodium berghei** --genetics--GE; Species Specificity; Transcription, Genetic

Molecular Sequence Databank No.: GENBANK/M19172; GENBANK/M19173

CAS Registry No.: 0 (Oligonucleotides); 0 (Plasmids); 0 (RNA, Ribosomal); 0 (RNA, Ribosomal, 18S)

Enzyme No.: EC 3.1.- (Endonucleases); EC 3.1.30.1 (Aspergillus Nuclease S1)

Record Date Created: 19880712

7539562 93064842 PMID: 1359498

Identification and quantification of rodent malaria strains and species using gene probes.

Snounou G; Bourne T; Jarra W; Viriyakosol S; Brown K N

Division of Parasitology, National Institute for Medical Research, Mill Hill, London.

Parasitology (ENGLAND) Aug 1992, 105 (Pt 1) p21-7, ISSN 0031-1820 Journal Code: 0401121

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A DNA probe PCsv4 and a subclone thereof PCsv4.1, hybridize specifically to rodent malaria DNA. DNA purified from a small volume (10 microliters) of infected mouse blood was used to determine the composition of the parasite population present. The hybridization signal following PCsv4 probing of slot-blotted DNA correlated directly with parasitaemia. The hybridization pattern and intensity, resulting from probing restriction enzyme digested and Southern-blotted genomic DNA, determined the identity of the infecting parasite line(s), and provided a semi-quantitative measure of parasite burden. Fifteen parasite lines representative of all four Plasmodium species infecting rodents can be differentiated in this way.

Tags: Animal; Male

Descriptors: *DNA Probes; *DNA, Protozoan--analysis--AN; *Malaria --parasitology--PS; *Plasmodium--classification--CL; Autoradiography; Blotting, Southern; Deoxyribonuclease EcoRI; Disease Models, Animal; Mice; Mice, Inbred CBA; **Nucleic** Acid **Hybridization** ; Plasmodium--genetics--GE; **Plasmodium berghei** --classification--CL; Plasmodium berghei--genetics--GE ; Plasmodium chabaudi--classification--CL; Plasmodium chabaudi--genetics --GE; Plasmodium yoelii--classification--CL; Plasmodium yoelii--genetics --GE; Polymorphism, Restriction Fragment Length; Regression Analysis; Restriction Mapping

CAS Registry No.: 0 (DNA Probes); 0 (DNA, Protozoan)

Enzyme No.: EC 3.1.21.- (Deoxyribonuclease EcoRI)

Record Date Created: 19921214

Conserved location of genes on polymorphic chromosomes of four species of malaria parasites.

Janse C J; Carlton J M; Walliker D; Waters A P
Laboratory for Parasitology, University of Leiden, The Netherlands.

Molecular and biochemical parasitology (NETHERLANDS) Dec 1994, 68 (2) p285-96, ISSN 0166-6851 Journal Code: 8006324
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The number of chromosomes and the chromosomal location and linkage of more than 50 probes, mainly of genes, have been established in four species of Plasmodium which infect African murine rodents. We expected that the location and linkage of genes would not be conserved between these species of malaria parasites since extensive inter- and intraspecific size differences of the chromosomes existed and large scale internal rearrangements and chromosome translocations in parasites from laboratory lines had been reported. Our study showed that all four species contained 14 chromosomes, ranging in size between 0.5 and 3.5 Mb, which showed extensive size polymorphisms. The location and linkage of the genes on the polymorphic chromosomes, however, was conserved and nearly identical between these species. These results indicate that size polymorphisms of the chromosomes are more likely due to variation in non-coding (subtelomeric, repeat) sequences and show that a high plasticity of internal regions of chromosomes that may exist does not frequently affect chromosomal location and linkage of genes.

Tags: Animal; Comparative Study; Support, Non-U.S. Gov't
Descriptors: *Chromosome Mapping; *Chromosomes--genetics--GE; *Genes, Protozoan--genetics--GE; *Malaria--parasitology--PS; *Plasmodium--genetics --GE; Electrophoresis, Gel, Pulsed-Field; Gene Rearrangement; Linkage (Genetics); Mice; Molecular **Probes** ; **Plasmodium** berghei--genetics--GE; Plasmodium chabaudi--genetics--GE; Plasmodium yoelii--genetics--GE; Polymorphism (Genetics)
CAS Registry No.: 0 (Molecular Probes)
Record Date Created: 19950602

Localization of ribosomal RNA and Pbs21-mRNA in the sexual stages of Plasmodium berghei using electron microscope in situ hybridization.

Shaw M K; Thompson J; Sinden R E

Molecular and Cellular Parasitology Group, Department of Biology, Imperial College of Science, Technology and Medicine, London/United Kingdom.

European journal of cell biology (GERMANY) Nov 1996, 71 (3) p270-6, ISSN 0171-9335 Journal Code: 7906240

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A reproducible technique for the ultrastructural localization of RNAs in malaria parasites has been developed which combines excellent structural preservation with high hybridization signals. Signals obtained following in situ hybridization with an antisense rRNA probe which recognizes all forms of small subunit (SSU) rRNA correlate with the density of ribosomes in the parasite cytoplasm and show that a) the male gametocyte has only 12 to 25% the ribosomes found in the female cell and asexual parasite and b) the probe did not hybridize with an electron-dense nuclear body previously called a nucleolus. We suggest this structure is either a transcription-, or a replication-factory. Using a probe for the sexual stage-specific protein Pbs21 mRNA, signal was found only in female gametocytes, zygotes and ookinetes and showed a non-random, clumped cytoplasmic distribution. It is not known at present whether the non-random distribution of the Pbs 21 mRNA is critical to the very delayed translation of the Pbs21 message into protein, which occurs only in the zygote and ookinete.

Tags: Animal; Female; Male; Support, Non-U.S. Gov't

Descriptors: *Antigens, Protozoan--genetics--GE; *Plasmodium berghei --genetics--GE; *Protozoan Proteins--genetics--GE; *RNA, Messenger --chemistry--CH; *RNA, Ribosomal--chemistry--CH; In Situ **Hybridization** ; **Plasmodium** berghei--growth and development--GD

CAS Registry No.: 0 (Antigens, Protozoan); 0 (Protozoan Proteins); 0 (RNA, Messenger); 0 (RNA, Ribosomal); 0 (ookinete surface antigen Pbs21, Plasmodium)

Record Date Created: 19970505

Plastid **origin of an extrachromosomal DNA molecule from** Plasmodium **, the causative agent of** malaria **.**

Howe C J
Department of Biochemistry, University of Cambridge, U.K.

Journal of theoretical biology (ENGLAND) Sep 21 1992, 158 (2) p199-205, ISSN 0022-5193 Journal Code: 0376342
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Several species of Plasmodium have been shown to contain a circular extrachromosomal DNA molecule which is widely supposed to be mitochondrial DNA. However, it has recently been shown to have a number of features in common with chloroplast DNA. Here, a phylogenetic analysis of RNA polymerase coding sequences from the Plasmodium molecule has been carried out using distance matrix, maximum likelihood, parsimony and operator invariant methods. The analysis indicates that the molecule is in fact derived from an oxygenic photosynthetic organism and should be regarded as plastid DNA. This suggests that Plasmodium originated from a phototroph that has lost the capacity to photosynthesize.

Tags: Animal; Support, Non-U.S. Gov't
Descriptors: *Chloroplasts--physiology--PH; *DNA-Directed RNA Polymerase --genetics--GE; *Phylogeny; *Plasmids--genetics--GE; *Plasmodium falciparum --genetics--GE; Amino Acid Sequence; Base Sequence; Photosynthesis --genetics--GE; Sequence Alignment
CAS Registry No.: 0 (Plasmids)

oodstream stages of Plasmodium berghei: evolutionary implications.

Gunderson J H; McCutchan T F; Sogin M L

Journal of protozoology (UNITED STATES) Nov 1986, 33 (4) p525-9, ISSN 0022-3921 Journal Code: 2985197R

Contract/Grant No.: GM32964; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

We have determined the complete nucleotide sequence of the coding region of the small subunit rRNA gene expressed by bloodstream stages of the apicomplexan Plasmodium berghei. It is 2059 nucleotides long. Elements contributing to its relatively large size are all concentrated in regions known to be variable in length among eukaryotes. In a phylogenetic tree constructed from pairwise comparisons of eukaryotic small subunit rRNA sequences, the apicomplexan line branches at a rather early point in eukaryotic evolution before any multicellular kingdoms had yet appeared.

Tags: Animal; Comparative Study; Support, U.S. Gov't, P.H.S.

Descriptors: Genes; * **Plasmodium berghei** --genetics--GE; * **RNA** , Ribosomal--genetics--GE; Base Sequence; Evolution; Phylogeny

Molecular Sequence Databank No.: GENBANK/M14599

CAS Registry No.: 0 (RNA, Ribosomal)

Record Date Created: 19870205

Localization of ribosomal RNA and Pbs21-mRNA in the sexual stages of Plasmodium berghei using electron microscope in situ hybridization.

Shaw M K; Thompson J; Sinden R E

Molecular and Cellular Parasitology Group, Department of Biology, Imperial College of Science, Technology and Medicine, London/United Kingdom.

European journal of cell biology (GERMANY) Nov 1996, 71 (3) p270-6, ISSN 0171-9335 Journal Code: 7906240

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A reproducible technique for the ultrastructural localization of RNAs in malaria parasites has been developed which combines excellent structural preservation with high hybridization signals. Signals obtained following in situ hybridization with an antisense rRNA probe which recognizes all forms of small subunit (SSU) rRNA correlate with the density of ribosomes in the parasite cytoplasm and show that a) the male gametocyte has only 12 to 25% the ribosomes found in the female cell and asexual parasite and b) the probe did not hybridize with an electron-dense nuclear body previously called a nucleolus. We suggest this structure is either a transcription-, or a replication-factory. Using a probe for the sexual stage-specific protein Pbs21 mRNA, signal was found only in female gametocytes, zygotes and ookinetes and showed a non-random, clumped cytoplasmic distribution. It is not known at present whether the non-random distribution of the Pbs 21 mRNA is critical to the very delayed translation of the Pbs21 message into protein, which occurs only in the zygote and ookinete.

Tags: Animal; Female; Male; Support, Non-U.S. Gov't

Descriptors: *Antigens, Protozoan--genetics--GE; *Plasmodium berghei --genetics--GE; *Protozoan Proteins--genetics--GE; *RNA, Messenger --chemistry--CH; *RNA, Ribosomal--chemistry--CH; In Situ **Hybridization** ; **Plasmodium** berghei--growth and development--GD

CAS Registry No.: 0 (Antigens, Protozoan); 0 (Protozoan Proteins); 0 (RNA, Messenger); 0 (RNA, Ribosomal); 0 (ookinete surface antigen Pbs21, Plasmodium)

Inhibition of Plasmodium **falciparum protein synthesis. Targeting the** plastid **-like organelle with thiostrepton.**

McConkey G A; Rogers M J; McCutchan T F

Growth and Development Section, Laboratory of Parasitic Diseases, NIAID, National Institutes of Health, Bethesda, Maryland 20892-0425, USA.

Journal of biological chemistry (UNITED STATES) Jan 24 1997, 272 (4) p2046-9, ISSN 0021-9258 Journal Code: 2985121R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The human malaria parasite Plasmodium falciparum has two extrachromosomal DNAs associated with organelles whose function is unclear. Both genomes encode ribosomal RNAs (rRNAs) that are distinct from the nuclear-encoded rRNAs. Secondary structure analysis of all the P. falciparum rRNAs indicates that only the large subunit (LSU) rRNA encoded by the plastid-like genome is the target for thiostrepton. Indeed we find that thiostrepton inhibits growth of the parasite in the micromolar range which is 10-fold below concentrations with observable effects on total protein synthesis. We have further examined selective effects of thiostrepton on the plastid function by comparing differential effects of the drug on cytoplasmic and organellar encoded transcripts. Treatment with either thiostrepton or rifampin, an inhibitor of organellar and eubacterial RNA polymerase, both showed disappearance of organellar-encoded RNA transcripts within 6 h of treatment while transcripts of a nuclear-encoded mRNA remained constant for at least 8 h of treatment. Hence, we show a selective effect on organelle function that is suggestive of interference in the protein synthesis apparatus of the plastid. Sensitivity of P. falciparum to thiostrepton confirms that the plastid-like genome is essential for the erythrocytic cycle and presents a novel therapeutic site for this class of antibiotics.

Tags: Animal; Support, U.S. Gov't, P.H.S.

tRNA genes transcribed from the plastid -like DNA of Plasmodium falciparum.

Preiser P; Williamson D H; Wilson R J

Division of Parasitology, National Institute for Medical Research, Mill Hill, London, UK.

Nucleic acids research (ENGLAND) Nov 11 1995, 23 (21) p4329-36, ISSN 0305-1048 Journal Code: 0411011

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Besides their mitochondrial genome, malarial parasites contain a second organellar DNA. This 35 kb circular molecule has a number of features reminiscent of plastid DNAs. Sequence analysis shows that along with other genes the circle codes for 25 different tRNAs all of which are transcribed. Six of the tRNAs have some unusual features, and one has an intron, the only one found so far on the circle. Comparison of codon and anticodon usage indicates that the 25 tRNAs are sufficient to decode all the protein genes present on the circle. The maintenance of such a parsimonious but complete translation system is further evidence for the functionality of the circle.

Tags: Animal; Support, Non-U.S. Gov't

Descriptors: *DNA, Protozoan--genetics--GE; *Genes, Protozoan; *Plasmodium falciparum--genetics--GE; *Plastids--genetics--GE; *RNA, Transfer--genetics--GE; *Transcription, Genetic; Anticodon; Base Sequence; DNA Primers; DNA, Circular--genetics--GE; Genetic Code; Molecular Sequence Data; Nucleic Acid Conformation; RNA, Messenger--analysis--AN; RNA, Protozoan--genetics--GE

Molecular Sequence Databank No.: GENBANK/X90351; GENBANK/X90352; GENBANK/X90353; GENBANK/X90354

CAS Registry No.: 0 (Anticodon); 0 (DNA Primers); 0 (DNA, Circular); 0 (DNA, Protozoan); 0 (RNA, Messenger); 0 (RNA, Protozoan); 9014-25-9 (RNA, Transfer)

Record Date Created: 19960117

A one-step lysis procedure for 18S ribosomal RNA-based diagnosis of infection by Plasmodium species.

Das A; Lal A A; Talwar G P; Hasnain S E; Sinha S
National Institute of Immunology, Aruna Asaf Ali Marg, New Delhi, India.

Analytical biochemistry (UNITED STATES) Oct 15 1996, 241 (2) p262-4,
ISSN 0003-2697 Journal Code: 0370535
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Tags: Animal; Human; Support, U.S. Gov't, Non-P.H.S.
Descriptors: Malaria--diagnosis--DI; * **Plasmodium berghei** --genetics--GE;
* **RNA** , Ribosomal, 18S--genetics--GE; Nucleic Acid Hybridization
CAS Registry No.: 0 (RNA, Ribosomal, 18S)
Record Date Created: 19970212

Evolutionary relatedness of Plasmodium species as determined by the structure of DNA.

McCutchan T F; Dame J B; Miller L H; Barnwell J

Science (UNITED STATES) Aug 24 1984, 225 (4664) p808-11, ISSN 0036-8075 Journal Code: 0404511
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Malaria parasites can be grouped evolutionarily by analysis of DNA composition and genome arrangement. Those that vary widely with regard to host range, morphology, and biological characteristics fit into only a small number of distinctive groups. The DNA of the human parasite Plasmodium falciparum fits into a group that includes rodent and avian malarias and is unlike the DNA of other primate malaria parasites. The DNA of Plasmodium vivax, which is also a human parasite, fits into a distinctly different group that includes Plasmodium cynomolgi, a parasite of monkeys. The evolutionary lines suggested here appear to be consistent with similarities seen among malaria parasites with regard to gene sequence.

Tags: Animal; Comparative Study
Descriptors: *DNA--analysis--AN; *Evolution; *Plasmodium--classification --CL; Base Composition; Base Sequence; Deoxycytidine--analysis--AN; Deoxyguanosine--analysis--AN; **Nucleic** Acid **Hybridization** ; Plasmodium --genetics--GE; **Plasmodium berghei** --classification--CL; Plasmodium berghei--genetics--GE; Plasmodium falciparum--classification--CL; Plasmodi um falciparum--genetics--GE; Plasmodium vivax--classification--CL; Plasmodium vivax--genetics--GE; Species Specificity
CAS Registry No.: 9007-49-2 (DNA); 951-77-9 (Deoxycytidine); 961-07-9 (Deoxyguanosine)
Record Date Created: 19840924

Differentiation of Toxoplasma gondii from closely related coccidia by riboprint analysis and a surface antigen gene polymerase chain reaction.

Brindley P J; Gazzinelli R T; Denkers E Y; Davis S W; Dubey J P; Belfort R; Martins M C; Silveira C; Jamra L; Waters A P; et al

Laboratory of Parasitic Diseases, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland.

American journal of tropical medicine and hygiene (UNITED STATES) Mar 1993, 48 (3) p447-56, ISSN 0002-9637 Journal Code: 0370507

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: AIM; INDEX MEDICUS

The tachyzoite of the human pathogen Toxoplasma gondii is morphologically indistinguishable from the proliferative stages of some other zoonotic coccidia, including Sarcocystis. To determine the identity of such coccidia obtained from human tissues and other sources, we compared riboprints (through restriction enzyme analysis of the polymerase chain reaction [PCR]-amplified small subunit rRNA gene) of the following protozoa: the RH and ts-4 strains of T. gondii, lines OH3 and S11, which are two recently isolated T. gondii-like parasites from Brazil, Neospora caninum, Sarcocystis species, and the malarial parasite Plasmodium berghei. In addition, the protozoan genomes were examined by PCR for homologs of surface antigen genes of T. gondii, and by Southern hybridization to the heterologous rRNA gene probe pSM 389. Strains OH3, S11, ts-4, and RH shared identical riboprints, and OH3, S11, and ts-4 have p22 and p30 surface antigen gene structures similar to RH. In contrast, riboprints for N. caninum and T. gondii differ with respect to Dde 1 sites, and moreover, their genomes vary significantly from one another at both the p22 and p30 gene loci. The riboprints of Sarcocystis and P. berghei differ markedly from T. gondii and N. caninum and from each other. Bam HI pSM 389 restriction fragment length polymorphisms differentiate ts-4 from RH, OH3, and S11. Our results confirm that OH3 and S11 are indeed T. gondii, but that N. caninum and T. gondii are likely to be separate species, thereby resolving previous uncertainties concerning the identity of these parasites. Together, the variation in riboprints and surface antigen gene structure reflects the phylogenetic diversity among these coccidia, and in addition, confirms the value of riboprinting in the identification of apicomplexan parasites such as T. gondii.

Tags: Animal; Comparative Study; Human; Support, U.S. Gov't, P.H.S.

Descriptors: *Antigens, Protozoan--genetics--GE; *RNA, Protozoan --genetics--GE; *RNA, Ribosomal--genetics--GE; *Toxoplasma--isolation and purification--IP; Antigens, Surface--genetics--GE; Apicomplexa--genetics --GE; Apicomplexa--immunology--IM; Apicomplexa --isolation and purification--IP; Base Sequence; Blotting, Southern; DNA, Protozoan --analysis--AN; DNA, Protozoan--chemistry--CH; DNA, Ribosomal--analysis --AN; DNA, Ribosomal--chemistry--CH; Molecular Sequence Data; **Nucleic Acid Hybridization** ; **Plasmodium** berghei--genetics--GE; **Plasmodium berghei** --immunology--IM; Plasmodium berghei--isolation and purification --IP; Polymerase Chain Reaction; Restriction Mapping; Sarcocystis--genetics --GE; Sarcocystis--immunology--IM; Sarcocystis --isolation and purification--IP; Swine; Toxoplasma--genetics--GE; Toxoplasma--immunology --IM

CAS Registry No.: 0 (Antigens, Protozoan); 0 (Antigens, Surface); 0 (DNA, Protozoan); 0 (DNA, Ribosomal); 0 (RNA, Protozoan); 0 (RNA,

Sequence alignment

```
Qy      61 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAAGATTAGCC 120
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Db     533 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAAGATTAGCC 474

Qy     121 TGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTATTAAATAATTATCG 180
           ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     473 TGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATCATTAAATAATTATCG 414

Qy     181 GATCATTAAGACCGACATTAATCTCTGTTTAATTTGTAAATTTTACAGTTAATTATATAT 240
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     413 GATCATTAAGACCGACATTAATCTCTGTTTAATTTGTTAATTTTACAGTTAATTATATAT 354

Qy     241 TTATCTTTATATAATAAATATAACATTGTACACCTCCGTTTTTATATAGGAGGAGACCGC 300
           |||||||||||||| | ||||||| |||||| |||||||||||||||||||||||||||||
Db     353 ATATCTTTATATAACATATATAACTTTGTACTCCTCCGTTTTTATATAGGAGGAGACCGC 294

Qy     301 CCCAGTCAAACTATCTTATAAATATTGTTAAAAATTTTGTTATAAAAATTTTATAAGAAT 360
           ||||||||||||||||||||||| ||||||||| ||||||| |||| |||| |||||||
Db     293 CCCAGTCAAACTATCTTATAAATACTGTTAAAAAATTTGTTA-AAAATTTTTTTAAGAAT 235

Qy     361 TTATATATATATAAAATGGTATTTCATTAACAATTACATTATTTCCAAAAAAATAATATT 420
           |||||||||||| ||||||||||||||| |||||||| ||||||||||||||||||||||
Db     234 TTATATATATAAAAAATGGTATTTCATTTACAATTACACTATTTCCAAAAAAATAATATC 175

Qy     421 ACTACTTCCCATTTATTCTATGTTATATATATATATTTTCAATATCTATTAATAGTAAAG 480
           | || |||||||||||| ||||| | ||||||||||||||||||||||||| |||||||||
Db     174 ATTATTTCCCATTTATGCTATGCTCTATATATATATTTTCAATATCTATTCATAGTAAAG 115

Qy     481 CTTCATAGGGTCTTTCTGTCCTAATATAAGAAATCTGCATCTTCACAGATAATTTTATTT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     114 CTTCATAGGGTCTTTCTGTCCTAATATAAGAAATCTGCATCTTCACAGATAATTTTATTT 55

Qy     541 CATTAAGATTTTTTTTAAGACAGCATTTAAGTCGTTACATCTTTCATGCAGGTC 594
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      54 CATTAAGATTTTTTTTAAGACAGCATTTAAGTCGTTACATCTTTCATGCAGGTC 1
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RESULT 7
PFLSRRN/c
LOCUS PFLSRRN 2700 bp DNA linear INV 27-SEP-1995
DEFINITION Plasmodium falciparum gene for a large subunit ribosomal RNA from the inverted repeat within the 35-Kb circular DNA.
ACCESSION X61660
VERSION X61660.1 GI:13318
KEYWORDS inverted repeat; ribosomal RNA; ribosomal RNA large subunit.
SOURCE malaria parasite P. falciparum.
ORGANISM Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 2700)
AUTHORS Gardner,M.J.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-1991) M.J. Gardner, Div of Parasitology, National Inst for Medical Research, The Ridgeway - Mill Hill, London NW7 1AA, UK
REFERENCE 2 (bases 1 to 2700)
AUTHORS Gardner,M.J., Feagin,J.E., Moore,D.J., Rangachari,K., Williamson,D.H. and Wilson,R.J.
TITLE Sequence and organization of large subunit rRNA genes from the extrachromosomal 35 kb circular DNA of the malaria parasite Plasmodium falciparum
JOURNAL Nucleic Acids Res. 21 (5), 1067-1071 (1993)
MEDLINE 93219063
FEATURES Location/Qualifiers
source 1. .2700
/organism="Plasmodium falciparum"
/strain="C10"
/db_xref="taxon:5833"
/dev_stage="Erythrocytic"
/clone="pf4, pf5, pf6a"
rRNA 1. .2700
/note="subcellular localisation unknown"
/product="large subunit rRNA"
BASE COUNT 1175 a 199 c 324 g 1002 t

ORIGIN

Query Match 91.4%; Score 543; DB 3; Length 2700;
Best Local Similarity 95.6%; Pred. No. 4.8e-66;
Matches 569; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

```
Qy       1 GTATCGCTTTAATAGGCGAACAGACTTACCCTTAAAACATACTACTGCCTTAGGATGCGA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2376 GTATCGCTTTAATAGGCGAACAGACTTACCCTTAAAACATACTACTGCTTTAGGATGCGA 2317

Qy      61 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAAGATTAGCC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2316 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAAGATTAGCC 2257

Qy     121 TGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTATTAAATAATTATCG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2256 TGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTACTAAATAATTATCG 2197

Qy     181 GATCATTAAGACCGACATTAATCTCTGTTTAATTTGTAAATTTTACAGTTAATTATATAT 240
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    2196 GATCATTAAGACCGACATTTATCTCTGTTTAATTTGTAAATTTTACAGTTAATTATATAT 2137

Qy     241 T-TATCTTTATATAATAAATATAACATTGTACACCTCCGTTTTTATATAGGAGGAGACCG 299
           | ||||||||||||||||||||||||||||||||| ||||||||| ||||||||||||||||
Db    2136 TATATCTTTATATAATAAATATAACATTGTACTCCTCCGTTTATATATAGGAGGAGACCG 2077

Qy     300 CCCCAGTCAAACTATCTTATAAATATTGTTAAAAATTTTGTTATAAAAATTTTATAAGAA 359
           |||||||||||||||| |||||||||||| |||| |||||||||||| || ||||||||
Db    2076 CCCCAGTCAAACTATCTCATAAATATTGTTTAAAAATTTGTTATAAAATTTCTATAAGAA 2017

Qy     360 TTTATATATATATAAAATGGTATTTCATTAACAATTACATTATTTCCAAAAAAATAATAT 419
           |||||||||| ||||||||||||||||||  || || |||||||||| ||||||||||||
Db    2016 TTTATATATAAATAAAATGGTATTTCATTTTTAACTAAATTATTTCCAAGAAAATAATAT 1957

Qy     420 TACTACTTCCCATTTATTCTATGTTATATATATATATTTTCAATATCTATTAATAGTAAA 479
           || |  |||||||||| |||||||| ||||||||||||||| ||| ||||||||||||||
Db    1956 TATTGTTTCCCATTTATACTATGTTAAATATATATATTTTCATTATTTATTAATAGTAAA 1897

Qy     480 GCTTCATAGGGTCTTTCTGTCCTAATATAAGAAATCTGCATCTTCACAGATAATTTTATT 539
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Db    1896 GCTTCATAGGGTCTTTCTGTCCTAATATAAGAAATCTGTATCTTCACAGATAATTTTATT 1837

Qy     540 TCATTAAGATTTTTTTTAAGACAGCATTTAAGTCGTTACATCTTTCATGCAGGTC 594
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1836 TCATTAAGATTTTTTTTAAGACAGCATTTAAGTCGTTACATCTTTCATGCAGGTC 1782
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RESULT 8
PFTRNA/c
LOCUS PFTRNA 5142 bp DNA circular INV 01-AUG-1994
DEFINITION P.falciparum gene for tRNA I,A,N,L,R,V,R,M,T.
ACCESSION X75545
VERSION X75545.1 GI:520908
KEYWORDS large ribosomal subunit; small ribosomal subunit RNA; transfer RNA-Ala; transfer RNA-Arg; transfer RNA-Asn; transfer RNA-Ile; transfer RNA-Leu; transfer RNA-Thr; transfer RNA-Val; trnA gene; trnI gene; trnL gene; trnM gene; trnN gene; trnR gene; trnT gene; trnV gene.
SOURCE malaria parasite P. falciparum.
ORGANISM Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 5142)
AUTHORS Gardner,M., Preiser,P., Rangachari,K., Moore,D., Feagin,D., Williamson,D.H. and Wilson,R.J.
TITLE Nine duplicated tRNA genes on the plastid-like DNA of the malaria parasite Plasmodium falciparum
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Sequence and organization of large subunit rRNA genes from the extrachromosomal 35 kb circular DNA of the malaria parasite *Plasmodium falciparum*

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ABSTRACT

The malaria parasite *Plasmodium falciparum* carries an extrachromosomal 35 kb circular DNA molecule of unknown provenance. A striking feature of the circle is a palindromic sequence of genes for subunit rRNAs and several tRNAs, spanning *ca.* 10.5 kb. The palindrome has an intriguing resemblance to the inverted repeat of plastid genomes, and the sequence and putative secondary structure of the malarial large subunit (LSU) rRNA described in this report were used as the basis of a phylogenetic study. The malarial rRNA was found to be highly divergent in comparison with a selected group of chloroplast LSU rRNAs but was more closely related to them than to mitochondrial LSU rRNA genes.

INTRODUCTION

Malaria parasites have two extrachromosomal DNA molecules (reviewed in (1)). The first comprises a 6 kb reiterated sequence (2) that specifies three mitochondrial proteins— cytochrome b and subunits I and III of cytochrome oxidase (3). It also encodes fragments of both small and large subunit (SSU and LSU) rRNA genes (4,5). Since, in addition, it is concentrated in a subcellular fraction enriched in mitochondria (6), it is believed to be of mitochondrial origin. The second extrachromosomal DNA is an (A+T)-rich (>80%) 35 kb circle whose organellar location and evolutionary origin remains to be established (7). The portion of the 35 kb circle that has been sequenced has two striking features, firstly, juxtaposed *rpo*B and *rpo*C genes with homology to those of *Escherichia coli* and chloroplasts (8), and secondly, a palindromic sequence comprising rRNA and tRNA genes that is reminiscent of the inverted repeat found in chloroplast genomes (9). These characteristics led us to propose that malaria parasites may have had a hitherto unsuspected photosynthetic ancestor (1), reviewed in (10). Here we report the sequence and predicted secondary structure of the LSU rRNA, as well as a phylogenetic analysis based on these data.

MATERIALS AND METHODS

DNA analysis

Isolation of the 35 kb circular DNA of *Plasmodium falciparum* and general procedures used in cloning and DNA sequencing have been described elsewhere (7,8). The IR_A end of the palindrome was obtained by conventional cloning (*Hind*III fragment 4 in Fig.2) and the IR_B end by PCR amplification from total *P.falciparum* DNA. The primers used for the latter purpose, 5′-CGTGAGACAGTTCGGTCC and 5′-CCCAAAATA-GATATGTTACC, were based on sequenced clones. The first primer sequence is located in *Hind*III fragment 4 near the 3′ end of the IR_A copy of the LSU rRNA gene and was expected to be repeated in the IR_B copy. The second, unique, primer was derived from a cloned fragment of *Hind*III fragment 2 (Fig.2), and was located about 1.5 kb downstream from the estimated 3′ end of the IR_B LSU rRNA gene. The resulting PCR-amplified product (*ca.* 2 kb) was cloned directly in the TA vector (Invitrogen) for sequencing. The sequences of the two 3′ ends of the LSU rRNA genes and adjacent downstream regions obtained in this way were determined using custom-made oligonucleotide primers. The 5′ and central portions of the LSU rRNA gene were determined by sequencing cloned copies of *Hind*III fragments 5 and 6a. The complete nucleotide sequence of the gene is deposited in the EMBL database under the accession number X61660.

RNA analyses

Procedures for RNA extraction, Northern blotting and transcript mapping have been described in detail elsewhere (7,8). Mapping of the 5′ end of the LSU transcript was carried out by primer extension using total RNA and an oligonucleotide sequence located 85 nucleotides down-stream from the presumptive 5′ end. The 3′ end was mapped by RNase protection, in which total RNA was hybridized with ^{32}P-labelled anti-sense transcripts made *in vitro* (5) from *Rsa*I or *Rsa*I/*Alu*I restriction fragments of cloned circular DNA containing the 3′ end of the LSU rRNA from IR_A. The hybrids were digested with RNase and electrophoresed on a 6% acrylamide, 7M urea sequencing gel.

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Phylogenetic analysis

The malarial LSU rRNA sequence was aligned visually with the predicted secondary structure of *E.coli* LSU rRNA (11), allowing us to identify stretches of conserved sequence (a total of 608 nt) suitable for phylogenetic analysis. The GCG sequence programme PILEUP (12) was used to align these fragments from the malarial gene with corresponding regions from the specified organisms. With this alignment the programmes DNADIST, NEIGHBOR and DRAWTREE from J.Felsenstien's PHYLIP 3.4 package (13) were used to compute distance matrices and construct an unrooted tree.

RESULTS

The palindrome

Purified 35 kb circular DNA digested with *Hind*III yielded seven bands whose stoichiometric proportions are illustrated in Fig.1. Densitometric and restriction analysis (not shown) revealed that band 5 comprised two copies of the same fragment. Likewise, band 6 comprised a doublet, resolved in some gels, each of the two constituent copies of which, labelled 6a and 6b, being present in duplicate molar amounts. Further restriction mapping and cloning has now allowed each palindromic arm to be separately identified and they have been dubbed IR_A and IR_B by analogy with those of chloroplast genomes (14). As shown schematically in Fig.2, each arm of the palindrome contains one SSU and one LSU rRNA gene and a cluster of intervening tRNA genes (indicated in Fig.2, but to be presented in detail elsewhere). This overall arrangement is consistent with the occurrence on the circles of a cruciform structure (15), and with the detection of rapidly renaturing (snap-back) fragments following denaturation of molecules cleaved at pairs of restriction sites located symmetrically across the region (16, and Gardner *et al.*, in preparation). We have shown that the sequence of the SSU rRNA is distinct from the nucleus-encoded SSU rRNA genes and that its inferred secondary structure is consistent with an organellar origin (7).

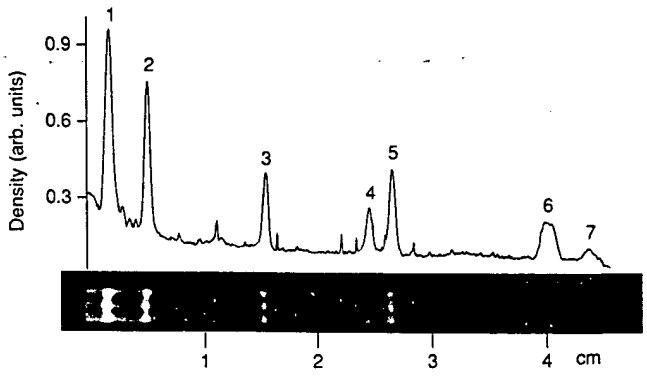

Figure 1. Densitometric analysis of a *Hind*III restriction digest of the 35 kb circular DNA from *P.falciparum*. The numbers were used in labelling the map shown in Fig.2. As discussed in the text, band 5 carries two molar copies of fragment 5. Band 6 is a doublet, resolved in some gels into two components, 6a and 6b, each of which is present in two molar copies.

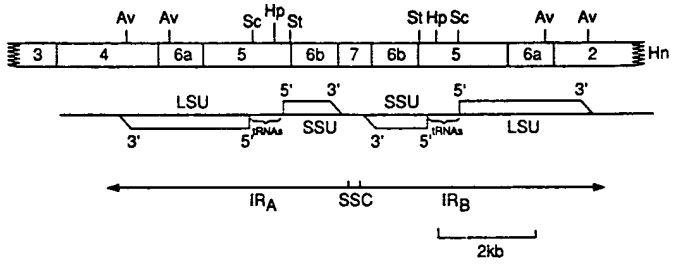

Figure 2. Schematic of the arrangement of the rRNA genes and restriction map in the palindromic segment of the malarial 35 kb circular DNA. The positions of two clusters of tRNAs are indicated. IR_A and IR_B denote the arms of the palindrome. *Av*, *Ava*II; *Sc*, *Sca*I; *Hp*, *Hpa*I; *St*, *Sty*I; *Hn*, *Hind*III. LSU, SSU, large and small rRNA subunits. SSC, small single copy sequence. Numbers in the bar are labels for the *Hind*III fragments (see Fig.1).

LSU rRNA sequence analysis

The predicted secondary structure of the LSU rRNA encoded by the *P.falciparum* 35 kb circular DNA is shown in Fig.3. It was derived from sequence assembled from cloned *Hind*III fragments 4, 5 and 6a (Fig.2). About 300 nt at the 3′ terminus of the IR_B copy (the limit of our cloned PCR-amplified sequence) was found to be identical in the two copies of the gene.

The format in Fig.3 is based on that of *E.coli* (11), capital letters being used to indicate bases conserved between the *P.falciparum* and *E.coli* sequences. The overall level of conservation is *ca.*40%, but in the core regions it averages 75% (5). Some portions of the molecule are extremely rich in A/U and may be idiosyncratic in their secondary structure; the putative helices indicated in these regions have not been substantiated structurally. As in bacterial and chloroplast LSU rRNAs, a possible helical structure exists between the 5′ and 3′ termini; this is indicated on both halves of Fig.3.

The complete DNA sequence of the LSU gene is deposited in the EMBL database under the accession number X61660.

Transcript analysis

Northern blots of total RNA extracted from parasitized erythrocytes probed with an oligonucleotide complementary to sequence near the 5′ end of the LSU rRNA revealed a single transcript of *ca.* 2.9 kb (data not shown). This transcript was somewhat larger than the size predicted from the LSU rRNA sequence alone (2694 nt). Its 5′ end was examined by primer extension (Fig.4A), and although it was not possible to read the sequence to the final nucleotide of the 85 nt extension product (see caret), the size of the transcript corresponded closely with that predicted from the secondary structure analysis. The 3′ end was determined from RNase protection studies using as probes ^{32}P-labelled *in vitro* transcripts complementary to the expected 3′ end of the LSU rRNA. Several protected products were detected using a probe corresponding to an 885 nt *Rsa*I fragment (Fig.4B); the largest product (244 nt) mapped to the LSU 3′ end predicted from the secondary structure. This fragment was the only one protected when the probe was shortened to include minimal sequence (*ca.*30 nt) 3′ of the predicted LSU end (Fig.4C), indicating that the fragments with estimated sizes of 110 nt, 76/78 nt and 63 nt were derived from transcripts of sequences downstream from the LSU rRNA gene, including the tRNA shown in Fig.4C.

Phylogenetic analysis

The LSU rRNA sequence was examined for phylogenetic information that might throw light on the provenance of the

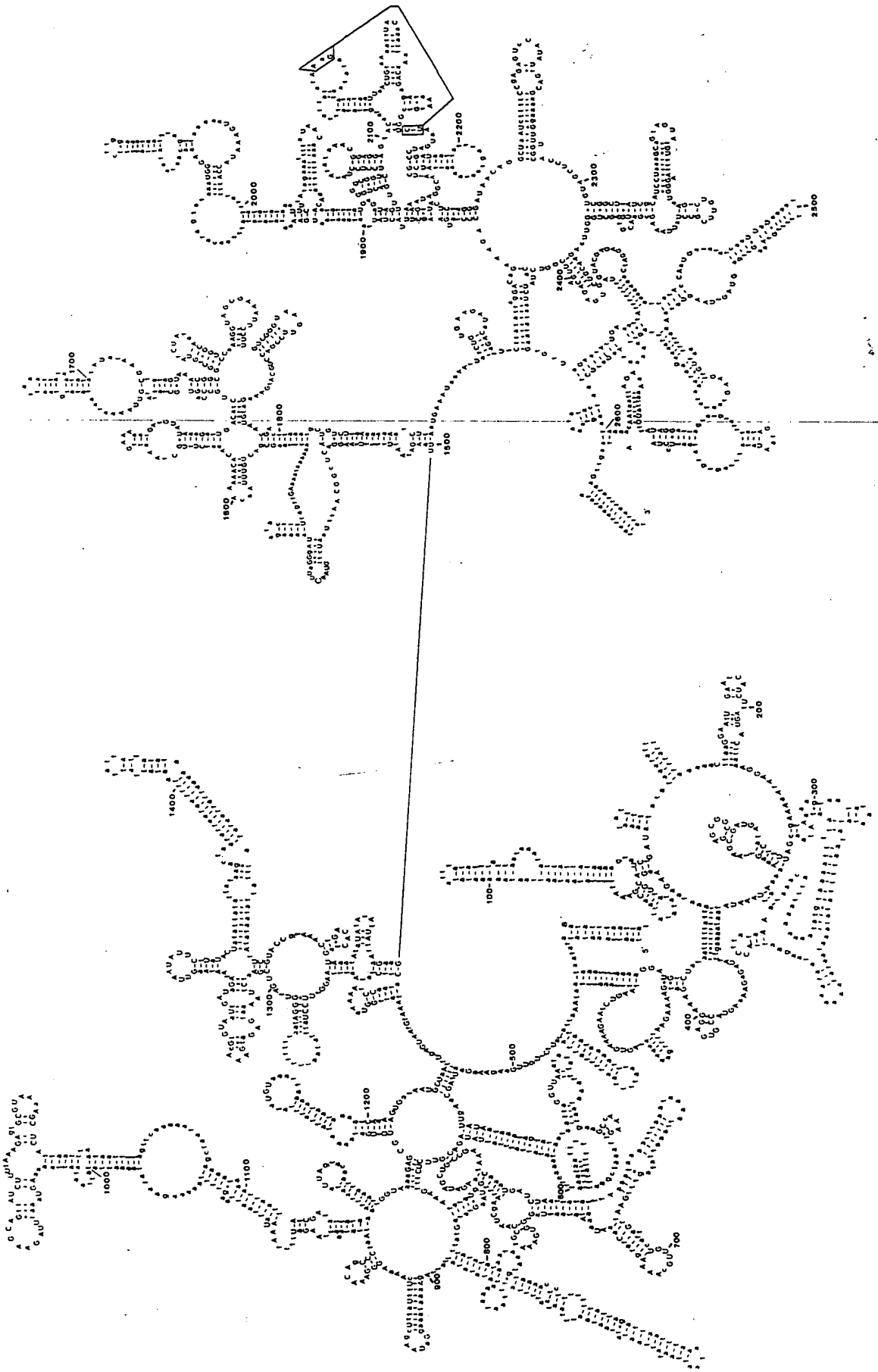

Figure 3. Predicted secondary structure of extrachromosomal, 35 kb circle, LSU rRNA of *P.falciparum* based on that of *E.coli* (11). Conserved bases are indicated in capital letters, parasite-specific positions are indicated with small letters for clarity, using t for uridine.

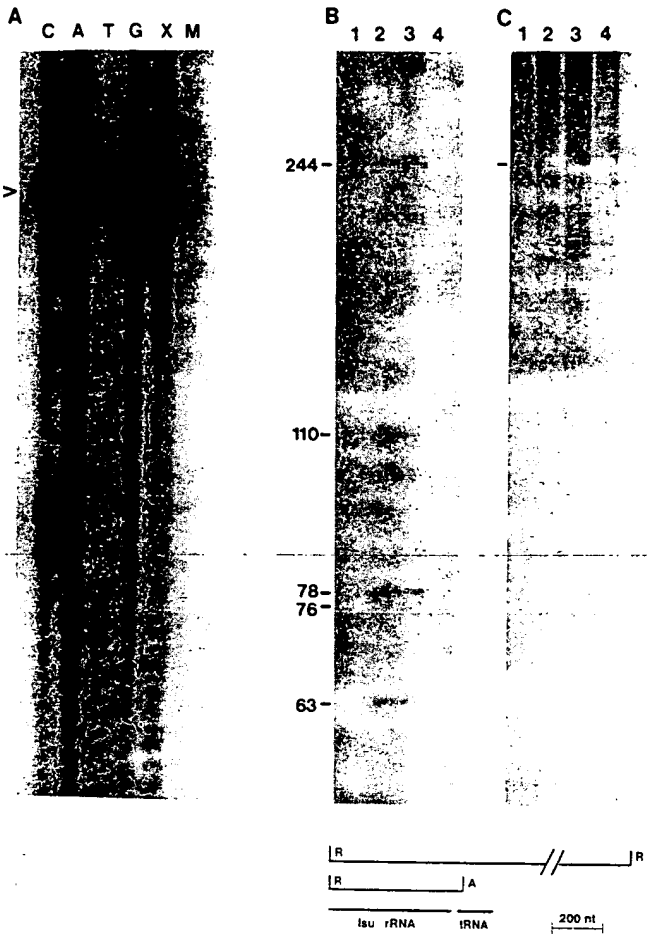

Figure 4. A. Determination of the 5′ end of the LSU rRNA. Total *P.falciparum* RNA was hybridized to an oligonucleotide complementary to sequences near the expected 5′ end of the LSU rRNA. Sequencing was by the dideoxy chain-termination method. No dideoxynucleotides were added to lane X and primer was omitted in lane M. The size of the major extension product (caret = 85 nt) was estimated from adjacent sequencing ladders. B. RNase protection study to determine the 3′ end of the LSU rRNA. Total *P.falciparum* RNA (5 and 10 μg in lanes 2 and 3, respectively) was hybridized with ^{32}P-labelled *in vitro* RNA transcripts complementary to the expected 3′ end of the LSU rRNA (*RsaI* fragment R/R) shown in the schematic map below panels B and C. The hybrids were digested with RNase and electrophoresed on a 6% acrylamide, 7M urea sequencing gel. Lanes 1 and 4 are controls with no RNA and 10μg of *Trypanosoma brucei* total RNA respectively, hybridized and digested as above. Approximate sizes of the protected fragments were estimated from end-labelled *HpaII* fragments of pBR322 and are indicated in nt. C. As in B, except that the ^{32}P-labelled *in vitro* transcript was produced from the *RsaI-AluI* fragment (R/A) shown in the schematic map.

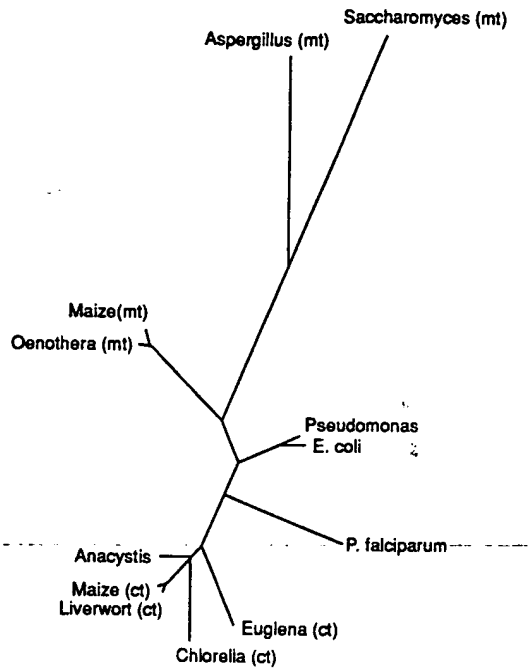

Figure 5. Phylogenetic analysis of the malarial 35 kb LSU rRNA (*Plasmodium falciparum*). An unrooted tree was computed using the PHYLIP 3.4 programmes DNA DIST, NEIGHBOR and DRAWTREE. The sequences are as follows; Eubacterial: *Pseudomonas aeruginosa* and *E.coli*. Cyanobacterial: *Anacystis nidulans*. Mitochondrial sequences of Maize (*Zea mays*), *Oenothera berteriana*, *Aspergillus nidulans* and *Saccharomyces cerevisiae* are designated 'mt'. Chloroplast sequences of Maize, Liverwort (*Marchantia polymorpha*), *Chlorella ellipsoidea* and *Euglena gracilis* are designated 'ct'.

Table 1. Sequence positions (*E.coli*) of LSU rRNA genes used for alignment (based on Gutell and Fox, reference 11)

026–034	0971–0984	1883–1891	2381–2394
188–205	1057–1073	1897–1905	2418–2435
240–259	1082–1098	1906–1918	2447–2455
447–460	1193–1202	1927–1940	2466–2478
497–514	1248–1256	1945–1955	2490–2505
560–579	1307–1316	1962–1971	2552–2582
580–588	1349–1367	1989–1995	2583–2589
664–677	1599–1613	2009–2023	2607–2617
745–753	1662–1677	2057–2065	2653–2667
773–794	1814–1826	2068–2081	2719–2728
799–812	1833–1843	2259–2275	2877–2883

circular DNA molecule. The 608 nt we used were selected from 44 segments (Table 1) from positions throughout the molecule including the most conserved portions (17). Using PILEUP, they were aligned with corresponding sequences from the eubacteria *Escherichia coli* and *Pseudomonas aeruginosa*, the cyanobacterium *Anacystis nidulans*, the chloroplast 23S ribosomal RNAs of *Zea mays*, *Marchantia polymorpha*, *Chlorella ellipsoidea* and *Euglena gracilis*, together with the corresponding mitochondrial genes from two plants *Zea mays* and *Oenothera berteriana* and two fungae, *Apergillus nidulans* and *Saccharomyces cerevisiae* (11). The PHYLIP programmes DNADIST and NEIGHBOR (18) were used to compute an unrooted tree (Fig.5). To infer a root, *E.coli* was taken as the outgroup, based on the considerable body of evidence indicating that mitochondria are of eubacterial origin (19). Our analysis thus indicates that although the malarial LSU rRNA was distantly related to all of the selected chloroplast sequences, it was more closely related to plastids than to mitochondria.

DISCUSSION

Although we have not completely sequenced both LSU rRNA genes within the palindrome, we have shown that the 3′ end is identical in both copies for at least 300 nt, and both restriction mapping (Fig.2) and denaturation studies (16 and Gardner *et al.*, unpublished observations) indicate that most probably the two

genes resemble each other. We therefore feel justified in commenting on various aspects of the LSU rRNA sequence presented here.

LSU rRNAs are frequently fragmented, with short regions at the 5′ and 3′ends separately encoded as 5.8S and 4.5S RNAs, respectively (11). We have found no evidence for the occurence of either of these two fragments, and the sequence reported here is continuous. This is in striking contrast to the LSU rRNA gene from *P.falciparum's* so-called '6 kb element', which is of mitochondrial origin. This gene is extensively fragmented and at the sequence level is essentially unrelated to its counterparts on the circle (5).

We have previously pointed out that the malarial 35 kb circular DNA resembles the residual plastid genome of non-photosynthetic plants (1,10), and the presence of the inverted repeat containing ribosomal RNA and tRNA genes was one feature leading us to this view. However, certain features of the repeat distinguish it from that found on the plastid genomes of higher plants and most algae (9): thus the LSU genes on the malarial circle are distal rather than proximal to the small single copy (SSC) region, the direction of transcription of the malarial LSU rRNA is away from the SSC rather than towards it, and the SSC in the malarial palindrome has been reduced substantially. In this last feature, however, the malarial circle is like the residual plastid genome of the non-photosynthetic plant *Epiphagus* in which most of the SSC region has also been deleted, leaving only two genes (20).

It was with this background that we conducted the phylogenetic analysis of the LSU gene reported here. The unrooted tree of Fig.5, based on the nearest neighbour model of Saitou and Nei (18) and LSU rRNAs from representative eubacteria, chloroplasts, and mitochondria, indicates that those from mitochondria are the most distantly related to the malarial gene. However, the malarial gene is also highly diverged from the chloroplast and cynaobacterial genes used in the analysis. Similar results have been obtained with phylogenetic analyses of the 35 kb circle *rpo*B gene (Gardner *et al.*,in preparation) and a portion of the *rpo*C gene (21), except that in both these instances the malarial gene was more firmly placed with those of chloroplasts than has been the case in the present analysis. Phylogenetic analyses by other workers of nucleus-encoded SSU rRNA genes confirmed earlier speculations that malaria parasites and related organisms (Phylum Apicomplexa) may have evolved from dinoflagellates (22–24). However, to the best of our knowledge, no DNA sequence information is available about the plastid genomes of photosynthetic dinoflagellates, and additional phylogenetic analyses with genes from this source and from other algae will probably be required before a definitive conclusion can be reached about the provenance of the malarial 35 kb circle.

In the meantime, we aim to complete the sequence of the malarial circular DNA, to localize it within the cell, and to gain insight into its function.

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